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(54) Title: MOLECULAR CARDIOTOXICOLOGY MODELING

(57) Abstract: The present invention is based on the elucidation of the global changes in gene expression and the identification of toxicity markers in tissues or cells exposed to a known cardiotoxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The invention includes a database of genes characterized by toxin-induced differential expression that is designed for use with microarrays and other solid-phase probes.



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**MOLECULAR CARDIOTOXICOLOGY MODELING**

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**RELATED APPLICATIONS**

[0001] This application claims priority to U.S. Application 10/338,044, filed January 8, 2003, which is a continuation-in-part of U.S. Application 10/191,803, filed June 10, 2002, which claims priority to U.S. Provisional Applications 60/303,819 filed on July 10, 2001; 60/305,623 filed on July 17, 2001; 60/369,351 filed on April 3, 2002; and 60/377,611 filed on May 6, 2002, all of which are herein incorporated by reference in their entirety.

[0002] This application is also related to U.S. Application Nos. 09/917,800; 10/060,087; 10/152,319; and 10/301,856, all of which are also herein incorporated by reference in their entirety.

**SEQUENCE LISTING SUBMISSION ON COMPACT DISC**

[0003] The Sequence Listing submitted concurrently herewith on compact disc under Section 801(a)(i) and under 37 C.F.R. §§ 1.821(c) and 1.821(e) is herein incorporated by reference in its entirety. Four copies of the Sequence Listing, one on each of four compact discs are provided. Copy 1, Copy 2 and Copy 3 are identical. Copies 1, 2 and 3 are also identical to the CRF. Each electronic copy of the Sequence Listing was created on January 7, 2004 with a file size of 3952 KB. The file names are as follows: Copy 1- gl 5090 01 wo.txt; Copy 2- gl 5090 01 wo.txt; Copy 3- gl 5090 01 wo.txt; and CRF- gl 5090 01 wo.txt.

**BACKGROUND OF THE INVENTION**

[0004] The need for methods of assessing the toxic impact of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism has led to the development of procedures which utilize living organisms as biological monitors. The simplest and most convenient of these systems utilize unicellular microorganisms such as yeast and bacteria, since they are the most easily maintained and manipulated. In addition, unicellular screening systems often use easily detectable changes in phenotype to monitor the effect of test compounds on the cell. Unicellular organisms, however, are inadequate models for estimating the potential effects of many compounds on complex multicellular animals, in

part because they do not have the ability to carry out biotransformations to the extent or at levels found in higher organisms.

[0005] The biotransformation of chemical compounds by multicellular organisms is a significant factor in determining the overall toxicity of agents to which they are exposed. Accordingly, multicellular screening systems may be preferred or required to detect the toxic effects of compounds. The use of multicellular organisms as toxicology screening tools has been significantly hampered, however, by the lack of convenient screening mechanisms or endpoints, such as those available in yeast or bacterial systems. In addition, previous attempts to produce toxicology prediction systems have failed to provide the necessary modeling data and statistical information to accurately predict toxic responses (*e.g.*, WO 00/12760, WO 00/47761, WO 00/63435, WO 01/32928, and WO 01/38579).

#### **DESCRIPTION OF THE TABLES**

[0006] Table 1 provides the GenBank Accession Number for each of the sequences of the invention (see [www.ncbi.nlm.nih.gov/](http://www.ncbi.nlm.nih.gov/)), as well as the corresponding SEQ ID NO. in the sequence listing filed with this application. The gene name and Unigene Cluster Title, if known, cardiotoxicity prediction model code and internal reference no. are also provided.

[0007] Table 2 lists and describes the metabolic pathways in which the genes of the invention are known to function.

[0008] Table 3 provides the LocusLink and Unigene names and descriptions for the human homologues of the genes listed in Tables 1 and 2.

[0009] Table 4 defines the model codes, each of which corresponds to a table in Tables 5A-5LL. Each of Tables 5A-5LL represents part of a cardiotoxicity prediction model and lists for each toxin, or class of toxins, the genes that are predictors of a toxic effect. For each gene listed, the mean and standard deviation for gene expression levels in Tox-Group and Non-tox Group samples, as well as the linear discriminant analysis score (LDA score), are indicated.

[0010] Table 5A lists the genes that predict a toxic effect in samples treated with adrenergic agonists.

[0011] Table 5B lists the toxicity prediction genes in samples treated with alkylating agents.

[0012] Table 5C lists the toxicity prediction genes in samples treated with adriamycin (120 and 168-hour time point data).

[0013] Table 5D lists the toxicity prediction genes in samples treated with adriamycin (6 and 24-hour time point data).

[0014] Table 5E lists the toxicity prediction genes in samples treated with amphotericin B.

[0015] Tables 5F and 5G list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with BI-QT, a proprietary heart and liver toxin.

[0016] Tables 5H and 5I list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with clenbuterol (24-hour time point data).

[0017] Tables 5J and 5K list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with clenbuterol (6-hour time point data).

[0018] Tables 5L and 5M list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with cyclophosphamide.

[0019] Tables 5N and 5O list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with epinephrine (24-hour time point data).

[0020] Tables 5P and 5Q list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with epinephrine (3 and 6-hour time point data).

[0021] Table 5R lists the toxicity prediction genes in samples treated with epirubicin.

[0022] Tables 5S and 5T list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with hydralazine.

[0023] Tables 5U and 5V list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with ifosfamide.

[0024] Tables 5W and 5X list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with isoproterenol (24-hour time point data).

[0025] Tables 5Y and 5Z list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with isoproterenol (3 and 6-hour time point data).

[0026] Tables 5AA and 5BB list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with minoxidil (3 and 6-hour time point data).

[0027] Tables 5CC and 5DD list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with norepinephrine (24-hour time point data).



[0028] Tables 5EE and 5FF list the toxicity prediction genes in an alternate model and in a core model, respectively, in samples treated with norepinephrine (3 and 6-hour time point data).

[0029] Tables 5GG (3-hour time point data) and 5HH (6 and 24-hour time point data) list the toxicity prediction genes in samples treated with phenylpropanolamine.

[0030] Table 5II lists the toxicity prediction genes in samples treated with rosiglitazone.

[0031] Tables 5JJ and 5KK list the toxicity prediction genes in a general model and in a general core model, respectively. The general model is produced by combining data from all the other models and includes, therefore, samples treated with various compounds and data taken at various time points. The general core model combines data from the core models produced using one toxin.

[0032] Table 5LL lists the toxicity prediction genes in samples treated with vasculature agents.

## **SUMMARY OF THE INVENTION**

[0033] The present invention is based, in part, on the elucidation of the global changes in gene expression in tissues or cells exposed to known toxins, in particular cardiotoxins, as compared to unexposed tissues or cells as well as the identification of individual genes that are differentially expressed upon toxin exposure.

[0034] In various aspects, the invention includes methods of predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, and predicting the cardiotoxicity of a compound. The invention also includes methods of identifying agents that modulate the onset or progression of a toxic response. Also provided are methods of predicting the cellular pathways that a compound modulates in a cell. The invention also includes methods of identifying agents that modulate protein activities.

[0035] In a further aspect, the invention includes probes comprising sequences that specifically hybridize to genes in Tables 1-5LL. Also included are solid supports comprising at least two of the previously mentioned probes. The invention also includes a computer system that has a database containing information identifying the expression level in a tissue or cell sample exposed to a cardiotoxin of a set of genes comprising at least two genes in Tables 1-5LL.

[0036] The invention further provides a core set of genes in Tables 5A-5LL from which probes can be made and attached to solid supports. These core genes serve as a preferred

set of markers of cardiotoxicity and can be used with the methods of the invention to predict or monitor a toxic effect of a compound or to modulate the onset or progression of a toxic response.

## DETAILED DESCRIPTION

[0037] Many biological functions are accomplished by altering the expression of various genes through transcriptional (*e.g.* through control of initiation, provision of RNA precursors, RNA processing, *etc.*) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death are often characterized by the variations in the expression levels of groups of genes.

[0038] Changes in gene expression are also associated with the effects of various chemicals, drugs, toxins, pharmaceutical agents and pollutants on an organism or cell(s). For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over-expression of oncogene/protooncogenes after exposure to an agent could lead to tumorigenesis or hyperplastic growth of cells (Marshall (1991), *Cell* 64: 313-326; Weinberg (1991), *Science* 254: 1138-1146). Thus, changes in the expression levels of particular genes (*e.g.* oncogenes or tumor suppressors) may serve as signposts for the presence and progression of toxicity or other cellular responses to exposure to a particular compound.

[0039] Monitoring changes in gene expression may also provide certain advantages during drug screening and development. Often drugs are screened for the ability to interact with a major target without regard to other effects the drugs have on cells. These cellular effects may cause toxicity in the whole animal, which prevents the development and clinical use of the potential drug.

[0040] The present inventors have examined tissue from animals exposed to known cardiotoxins which induce detrimental heart effects, to identify global changes in gene expression and individual changes in gene expression induced by these compounds. These global changes in gene expression, which can be detected by producing or obtaining gene expression profiles (an expression level of one or more genes), provide useful toxicity markers that can be used to monitor toxicity and/or toxicity progression by a test compound. Some of these markers may also be used to monitor or detect various disease or physiological states, disease progression, drug efficacy and drug metabolism.

### *Identification of Toxicity Markers*

[0041] To evaluate and identify gene expression changes that are predictive of toxicity, studies using selected compounds with well characterized toxicity have been conducted by the present inventors to catalogue altered gene expression during exposure *in vivo*. In the present study, cyclophosphamide, ifosfamide, minoxidil, hydralazine, BI-QT, clenbuterol, isoproterenol, norepinephrine, epinephrine, adriamycin, amphotericin B, epirubicin, phenylpropanolamine, and rosiglitazone were selected as known cardiotoxins. Cisplatin, PAN, dopamine, acyclovir, carboplatin, etoposide, temozolomide, vancomycin and compound delivery vehicles were selected as negative controls.

[0042] **Cyclophosphamide**, an alkylating agent, is highly toxic to dividing cells and is commonly used in chemotherapy to treat non-Hodgkin's lymphomas, Burkitt's lymphoma and carcinomas of the lung, breast, and ovary (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., p.1234, 1237-1239, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). Additionally, cyclophosphamide is used as an immunosuppressive agent in bone marrow transplantation and following organ transplantation. Though cyclophosphamide is therapeutically useful, it is also associated with cardiotoxicity, nephrotoxicity, and hemorrhagic cystitis. Once in the liver, cyclophosphamide is hydroxylated by the cytochrome P450 mixed function oxidase system. The active metabolites, phosphoramidate mustard and acrolein, cross-link DNA and cause growth arrest and cell death. Acrolein has been shown to decrease cellular glutathione levels (Dorr and Lagel (1994), *Chem Biol Interact* 93: 117-128).

[0043] The cardiotoxic effects of cyclophosphamide have been partially elucidated. One study analyzed plasma levels in 19 women with metastatic breast carcinoma who had been treated with cyclophosphamide, thiotepa, and carboplatin (Ayash *et al.* (1992), *J Clin Oncol* 10: 995-1000). Of the 19 women in the study, six developed moderate congestive heart failure. In another case study, a 10-year old boy, who had been treated with high-dose cyclophosphamide, developed cardiac arrhythmias and intractable hypotension (Tsai *et al.* (1990), *Am J Pediatr Hematol Oncol* 12: 472-476). The boy died 23 days after the transplantation.

[0044] Another clinical study examined the relationship between the amount of cyclophosphamide administered and the development of cardiotoxicity (Goldberg *et al.* (1986), *Blood* 68: 1114-1118). When the cyclophosphamide dosage was  $\leq 1.55$  g/m<sup>2</sup>/d, only 1 out of 32 patients had symptoms consistent with cyclophosphamide cardiotoxicity.

Yet when the dosage was greater than 1.55 g/m<sup>2</sup>/d, 13 out of 52 patients were symptomatic. Six of the high-dose patients died of congestive heart failure.

[0045] In a related study, Braverman *et al.* compared the effects of once daily low-dose administration of cyclophosphamide (87 +/- 11 mg/kg) and twice-daily high-dose treatment (174 +/- 34 mg/kg) on bone marrow transplantation patients (Braverman *et al.* (1991), *J Clin Oncol* 9: 1215-1223). Within a week, the high-dose patients had an increase in left ventricular mass index. Out of five patients who developed clinical cardiotoxicity, four were in the high-dose group.

[0046] **Ifosfamide**, an oxazaphosphorine, is an analog of cyclophosphamide. Whereas cyclophosphamide has two chloroethyl groups on the exocyclic nitrogen, ifosfamide contains one chloroethyl group on the ring nitrogen and the other on the exocyclic nitrogen. Ifosfamide is a nitrogen mustard and alkylating agent, commonly used in chemotherapy to treat testicular, cervical, and lung cancer, as well as sarcomas and lymphomas. Like cyclophosphamide, it is activated in the liver by hydroxylation, but it reacts more slowly and produces more dechlorinated metabolites and chloroacetaldehyde. Comparatively higher doses of ifosfamide are required to match the efficacy of cyclophosphamide.

[0047] Alkylating agents can cross-link DNA, resulting in growth arrest and cell death. Despite its therapeutic value, ifosfamide is associated with nephrotoxicity (affecting the proximal and distal renal tubules), urotoxicity, venoocclusive disease, myelosuppression, pulmonary fibrosis and central neurotoxicity (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., p.1234-1240, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). Ifosfamide can also cause acute severe heart failure and malignant ventricular arrhythmia, which may be reversible. Death from cardiogenic shock has also been reported (Cecil Textbook of Medicine 20<sup>th</sup> ed., Bennett *et al.* eds., p. 331, W.B. Saunders Co., Philadelphia, 1996).

[0048] Studies of patients with advanced or resistant lymphomas or carcinomas showed that high-dose ifosfamide treatment produced various symptoms of cardiac disease, including dyspnea, tachycardia, decreased left ventricular contractility and malignant ventricular arrhythmia (Quezado *et al.* (1993), *Ann Intern Med* 118: 31-36; Wilson *et al.* (1992), *J Clin Oncol* 19: 1712-1722). Other patient studies have noted that ifosfamide-induced cardiac toxicity may be asymptomatic, although it can be detected by electrocardiogram and should be monitored (Pai *et al.* (2000), *Drug Saf* 22:263-302).

[0049] **Minoxidil** is an antihypertensive medicinal agent used in the treatment of high blood pressure. It works by relaxing blood vessels so that blood may pass through them more easily, thereby lowering blood pressure. By applying minoxidil to the scalp, it has recently been shown to be effective at combating hair loss by stimulating hair growth. Once minoxidil is metabolized by hepatic sulfotransferase, it is converted to the active molecule minoxidil N-O sulfate (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., pp. 796-797, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). The active minoxidil sulfate stimulates the ATP-modulated potassium channel consequently causing hyperpolarization and relaxation of smooth muscle. Early studies on minoxidil demonstrated that following a single dose of the drug, patients suffering from left ventricular failure exhibited a slightly increased heart rate, a fall in the mean arterial pressure, a fall in the systemic vascular resistance, and a slight increase in cardiac index (Franciosa and Cohn (1981) *Circulation* 63: 652-657).

[0050] Some common side effects associated with minoxidil treatment are an increase in hair growth, weight gain, and a fast or irregular heartbeat. More serious side effects are numbness of the hands, feet, or face, chest pain, shortness of breath, and swelling of the feet or lower legs. Because of the risks of fluid retention and reflex cardiovascular effects, minoxidil is often given concomitantly with a diuretic and a sympatholytic drug.

[0051] While minoxidil is effective at lowering blood pressure, it does not lead to a regression of cardiac hypertrophy. To the contrary, minoxidil has been shown to cause cardiac enlargement when administered to normotensive animals (Moravec *et al.* (1994) *J Pharmacol Exp Ther* 269: 290-296). Moravec *et al.* examined normotensive rats that had developed myocardial hypertrophy following treatment with minoxidil. The authors found that minoxidil treatment led to enlargement of the left ventricle, right ventricle, and interventricular septum.

[0052] Another rat study investigated the age- and dose-dependency of minoxidil-induced cardiotoxicity (Herman *et al.* (1996) *Toxicology* 110: 71-83). Rats ranging in age from 3 months to 2 years were given varying amounts of minoxidil over the period of two days. The investigators observed interstitial hemorrhages at all dose levels, however the hemorrhages were more frequent and severe in the older animals. The 2 year old rats had vascular lesions composed of arteriolar damage and calcification.

[0053] **Hydralazine**, an antihypertensive drug, causes relaxation of arteriolar smooth muscle. Such vasodilation is linked to vigorous stimulation of the sympathetic nervous

system, which in turn leads to increased heart rate and contractility, increased plasma renin activity, and fluid retention (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., p. 794, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996).

The increased renin activity leads to an increase in angiotensin II, which in turn causes stimulation of aldosterone and sodium reabsorption.

**[0054]** Hydralazine is used for the treatment of high blood pressure (hypertension) and for the treatment of pregnant women suffering from high blood pressure (pre-eclampsia or eclampsia). Some common side effects associated with hydralazine use are diarrhea, rapid heartbeat, headache, decreased appetite, and nausea. Hydralazine is often used concomitantly with drugs that inhibit sympathetic activity to combat the mild pulmonary hypertension that can be associated with hydralazine usage.

**[0055]** In one hydralazine study, rats were given one of five cardiotoxic compounds (isoproterenol, hydralazine, caffeine, cyclophosphamide, or adriamycin) by intravenous injection (Kemi *et al.* (1996), *J Vet Med Sci* 58: 699-702). At one hour and four hours post-dose, early focal myocardial lesions were observed histopathologically. Lesions were observed in the rats treated with hydralazine four hours post-dose. The lesions were found in the inner one third of the left ventricular walls including the papillary muscles.

**[0056]** Another study compared the effects of isoproterenol, hydralazine and minoxidil on young and mature rats (Hanton *et al.* (1991), *Res Commun Chem Pathol Pharmacol* 71: 231-234). Myocardial necrosis was observed in both age groups, but it was more severe in the mature rats. Hypotension and reflex tachycardia were also seen in the hydralazine-treated rats.

**[0057]** BI-QT has been shown to induce QC prolongation in dogs and liver alterations in rats. Over a four week period, dogs treated with BI-QT exhibited sedation, decreased body weight, increased liver weight, and slightly increased levels of AST, ALP, and BUN. After three months of treatment, the dogs exhibited signs of cardiovascular effects.

**[0058]** Clenbuterol, a  $\beta_2$  adrenergic agonist, can be used therapeutically as a bronchial dilator for asthmatics. It also has powerful muscle anabolic and lipolytic effects. It has been banned in the United States but continues to be used illegally by athletes to increase muscle growth. In a number of studies, rats treated with clenbuterol developed hypertrophy of the heart and latissimus dorsi muscle (Doheny *et al.* (1998), *Amino Acids* 15: 13-25; Murphy *et al.* (1999), *Proc Soc Exp Biol Med* 221: 184-187; Petrou *et al.* (1995), *Circulation* 92: II483-II489).

[0059] In one study, mares treated with therapeutic levels of clenbuterol were compared to mares that were exercised and mares in a control group (Sleeper *et al.* (2002), *Med Sci Sports Exerc* 34: 643-650). The clenbuterol-treated mares demonstrated significantly higher left ventricular internal dimension and interventricular septal wall thickness at end diastole. In addition, the clenbuterol-treated mares had significantly increased aortic root dimensions, which could lead to an increased chance of aortic rupture.

[0060] In another study, investigators reported a case of acute clenbuterol toxicity in a human (Hoffman *et al.* (2001), *J Toxicol* 39: 339-344). A 28-year old woman had ingested a small quantity of clenbuterol, and the patient developed sustained sinus tachycardia, hypokalemia, hypophosphatemia, and hypomagnesemia.

[0061] Catecholamines are neurotransmitters that are synthesized in the adrenal medulla and in the sympathetic nervous system. Epinephrine, norepinephrine, and **isoproterenol** are members of the catecholamine sympathomimetic amine family (Casarett & Doull's Toxicology, The Basic Science of Poisons 6<sup>th</sup> ed., p. 618-619, C.D. Klaassen, Ed., McGraw Hill, New York, 2001). They are chemically similar by having an aromatic portion (catechol) to which is attached an amine, or nitrogen-containing group.

[0062] **Isoproterenol**, an antiarrhythmic agent, is used therapeutically as a bronchodilator for the treatment of asthma, chronic bronchitis, emphysema, and other lung diseases. Some side effects of usage are myocardial ischemia, arrhythmias, angina, hypertension, and tachycardia. As a  $\beta$  receptor agonist, isoproterenol exerts direct positive inotropic and chronotropic effects. Peripheral vascular resistance is decreased along with the pulse pressure and mean arterial pressure. However, the heart rate increases due to the decrease in the mean arterial pressure.

[0063] **Norepinephrine**, an  $\alpha$  and  $\beta$  receptor agonist, is also known as noradrenaline. It is involved in behaviors such as attention and general arousal, stress, and mood states. By acting on  $\beta$ -1 receptors, it causes increased peripheral vascular resistance, pulse pressure and mean arterial pressure. Reflex bradycardia occurs due to the increase in mean arterial pressure. Some contraindications associated with norepinephrine usage are myocardial ischemia, premature ventricular contractions (PVCs), and ventricular tachycardia.

[0064] **Epinephrine**, a potent  $\alpha$  and  $\beta$  adrenergic agonist, is used for treating bronchoconstriction and hypotension resulting from anaphylaxis as well as all forms of cardiac arrest. Injection of epinephrine leads to an increase in systolic pressure, ventricular contractility, and heart rate. Some side effects associated with epinephrine

usage are cardiac arrhythmias, particularly PVCs, ventricular tachycardia, renal vascular ischemia, increased myocardial oxygen requirements, and hypokalemia.

[0065] Anthracyclines are antineoplastic agents used commonly for the treatment of breast cancer, leukemias, and a variety of other solid tumors. However, the usefulness of the drugs are limited due dose-dependent cardiomyopathy and ECG changes (Casarett & Doull's Toxicology, The Basic Science of Poisons 6<sup>th</sup> ed., p. 619, C.D. Klaassen, Ed., McGraw Hill, New York, 2001).

[0066] **Adriamycin** (doxorubicin) is a cytotoxic anthracycline antiobiotic that inhibits the action of topoisomerase II. It has a wide spectrum of antitumor activity, however dose-related cardiotoxicity is a major side effect. The toxic effects are most likely due to the generation of free radicals (DeAtley *et al.* (1999), *Toxicology* 134: 51-62). In one study, rats were given a dose of either adriamycin alone or a dose of adriamycin following a dose of captopril (al-Shabanah *et al.* (1998), *Biochem Mol Biol Int* 45: 419-427). Those rats that were only given adriamycin developed myocardial toxicity after 24 hours manifested biochemically by an elevation of serum enzymes such as aspartate transaminase, lactate dehydrogenase, and creatine phosphokinase. The rats that were pre-treated with captopril exhibited a significant reduction in serum enzyme levels as well as restoration of white blood cell counts.

[0067] **Epirubicin** is a semisynthetic derivative of daunorubicin, an anthracycline, approved for the treatment of breast cancer (Casarett & Doull's Toxicology, The Basic Science of Poisons 6<sup>th</sup> ed., p. 619, C.D. Klaassen, Ed., McGraw Hill, New York, 2001). Yet, it, too, may induce cardiotoxicity. In one observational study, 120 patients with advanced breast cancer were followed before, during, and after treatment with epirubicin (Jensen *et al.* (2002), *Ann Oncol* 13: 699-709). Approximately 59% of the patients experienced a 25% relative reduction in left ventricular ejection fraction three years after epirubicin treatment, and of these patients 20% had deteriorated into having congestive heart failure.

[0068] **Amphotericin B** is a polyene, antifungal antibiotic used to treat fungal infections. Its clinical utility is limited by its nephrotoxicity and cardiotoxicity. Amphotericin B may depress myocardial contractility by blocking activation of slow calcium channels and inhibiting the influx of sodium ions (Casarett & Doull's Toxicology, The Basic Science of Poisons 6<sup>th</sup> ed., p. 621, C.D. Klaassen, Ed., McGraw Hill, New York, 2001). It has been shown to increase the permeability of the sarcolemmal membrane, and patients given



amphotericin B have developed ventricular tachycardia and cardiac arrest. This drug has been shown to induce cardiac arrest in rats as well. In the current study, amphotericin B led to an increase in serum Troponin T levels and some early signs of cardiomyopathy within 24 hours of one intravenous bolus injection.

[0069] **Phenylpropanolamine** was used in over-the-counter decongestants until recently, but was withdrawn when its association with cardiac deaths became known. It is both a beta-1 and alpha adrenergic receptor agonist and has been shown to induce cardiotoxicity in rats. In one rat study, phenylpropanolamine was shown to cause myocardial contractile depression without altering global coronary artery blood flow (Zaloga et al. (2000), *Crit Care Med* 28: 3679-3683).

[0070] In another study, rats were given single intraperitoneal doses of 1, 2, 4, 8, 16, or 32 mg/kg of phenylpropanolamine (Pentel et al. (1987), *Fundam Appl Toxicol* 9: 167-172). The animals exhibited dose-dependent increased blood pressure and, following termination, myocardial necrosis.

[0071] **Rosiglitazone** (Avandia) is a thiazolidinedione medication used to treat Type 2 diabetes. It reduces plasma glucose levels and glucose production and increases glucose clearance (Wagstaff and Goa (2002), *Drugs* 62: 1805-1837). Some side effects associated with rosiglitazone treatment are fluid retention, congestive heart failure, and liver disease. In patients who have heart failure or use insulin, there is a potential for mild-to-moderate peripheral edema with rosiglitazone treatment. It has been shown that patients that do not have heart failure or use insulin can also develop moderate-to-severe edema while using rosiglitazone (Niemeyer and Janney (2002), *Pharmacotherapy* 22: 924-929).

#### *Toxicity Prediction and Modeling*

[0072] The genes, gene expression information (including Tox Group means and standard deviations, Nontox Group means and standard deviations, and LDA scores) and gene expression profiles, as well as the portfolios and subsets of the genes provided in Tables 1-5LL, such as the core toxicity markers in Tables 5A-5LL, may be used to predict at least one toxic effect, including the cardiotoxicity of a test or unknown compound. As used herein, at least one toxic effect includes, but is not limited to, a detrimental change in the physiological status of a cell or organism. The response may be, but is not required to be, associated with a particular pathology, such as tissue necrosis, myocarditis, arrhythmias, tachycardia, myocardial ischemia, angina, hypertension, hypotension, dyspnea, and cardiogenic shock. Accordingly, the toxic effect includes effects at the molecular and

cellular level. Cardiotoxicity is an effect as used herein and includes but is not limited to the pathologies of tissue necrosis, myocarditis, arrhythmias, tachycardia, myocardial ischemia, angina, hypertension, hypotension, dyspnea, and cardiogenic shock. As used herein, a gene expression profile comprises any representation, quantitative or not, of the expression of at least one mRNA species in a cell sample or population and includes profiles made by various methods such as differential display, PCR, hybridization analysis, *etc.*

[0073] In general, assays to predict the toxicity or cardiotoxicity of a test agent (or compound or multi-component composition) comprise the steps of exposing a cell population to the test compound, assaying or measuring the level of relative or absolute gene expression of one or more of the genes in Tables 1-5LL and comparing the identified expression level(s) to the expression levels disclosed in the Tables and database(s) disclosed herein. Assays may include the measurement of the expression levels of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 50, 75, 100, 200, 500, 1000 or more genes from Tables 1-5LL, or ranges of these numbers, such as about 2-10, about 10-20, about 20-50, about 50-100, about 100-200, about 200-500 or about 500-1000 genes from Tables 1-5LL to create multi-gene expression profiles. Assays for toxicity prediction may also include the measurement of nearly all the genes in Tables 1-5LL. "Nearly all" or "substantially all" the genes or gene information may be considered to mean at least 80%, preferably 85%, 90% or 95%, of the genes or information in any one of or all of Tables 1-5LL.

[0074] The genes, gene expression information and databases of the present invention may also be used to predict the absence of a toxic effect, or the non-toxicity of a test compound. Gene expression profiles of cell or tissue samples from subjects or samples exposed to the test compound are prepared or obtained and then compared to those stored in a database of the invention. If the test sample gene expression profiles correlate with gene expression profiles classified as Non-tox Group samples, the test compound may be considered not to produce a toxic effect.

[0075] Further, the gene expression information and databases of the present invention may also be used to predict the dosage or level of exposure at which a particular test compound produces a toxic effect. Groups of human or animal subjects may be treated with varying dosages of a test compound for varying lengths of time, or cell or tissue samples may be taken from groups of human or animal subjects and treated with varying dosages of a test compound for varying lengths of time. Alternatively, human or animal

cell cultures may be exposed to varying dosages of a test compound for varying lengths of time. Gene expression profiles may then be prepared or obtained from the set of samples treated with the test compound. These gene expression profiles may subsequently be compared to gene expression profiles stored in a database of the invention. In the sample set, the lowest concentration or dosage of the test compound that produces a gene expression profile that matches a gene expression profile indicating a toxic effect (corresponding to one or more Tox-Group samples in the database) may be determined. This concentration or dosage may be considered to be the threshold level at or above which a toxic response or effect may be predicted.

[0076] In the methods of the invention, the gene expression level for a gene or genes induced by the test agent, compound or compositions may be comparable to the levels found in the Tables or databases disclosed herein if the expression level varies within a factor of about 2, about 1.5 or about 1.0 fold. In some cases, the expression levels are comparable if the agent induces a change in the expression of a gene in the same direction (*e.g.*, up or down) as a reference toxin.

[0077] The cell population that is exposed to the test agent, compound or composition may be exposed *in vitro* or *in vivo*. For instance, cultured or freshly isolated heart cells, in particular rat heart cells, may be exposed to the agent under standard laboratory and cell culture conditions. In another assay format, *in vivo* exposure may be accomplished by administration of the agent to a living animal, for instance a laboratory rat.

[0078] Procedures for designing and conducting toxicity tests in *in vitro* and *in vivo* systems are well known, and are described in many texts on the subject, such as Loomis *et al.*, Loomis's Essentials of Toxicology, 4th Ed., Academic Press, New York, 1996; Echobichon, The Basics of Toxicity Testing, CRC Press, Boca Raton, 1992; Frazier, editor, In Vitro Toxicity Testing, Marcel Dekker, New York, 1992; and the like.

[0079] In *in vitro* toxicity testing, two groups of test organisms are usually employed: one group serves as a control and the other group receives the test compound in a single dose (for acute toxicity tests) or a regimen of doses (for prolonged or chronic toxicity tests). Because, in some cases, the extraction of tissue as called for in the methods of the invention requires sacrificing the test animal, both the control group and the group receiving compound must be large enough to permit removal of animals for sampling tissues, if it is desired to observe the dynamics of gene expression through the duration of an experiment.

[0080] In setting up a toxicity study, extensive guidance is provided in the literature for selecting the appropriate test organism for the compound being tested, route of administration, dose ranges, and the like. Water or physiological saline (0.9% NaCl in water) is the solute of choice for the test compound since these solvents permit administration by a variety of routes. When this is not possible because of solubility limitations, vegetable oils such as corn oil or organic solvents such as propylene glycol may be used.

[0081] Regardless of the route of administration, the volume required to administer a given dose is limited by the size of the animal that is used. It is desirable to keep the volume of each dose uniform within and between groups of animals. When rats or mice are used, the volume administered by the oral route generally should not exceed about 0.005 ml per gram of animal. Even when aqueous or physiological saline solutions are used for parenteral injection, the volumes that are tolerated are limited, although such solutions are ordinarily thought of as being innocuous. The intravenous LD<sub>50</sub> of distilled water in the mouse is approximately 0.044 ml per gram and that of isotonic saline is 0.068 ml per gram of mouse. In some instances, the route of administration to the test animal should be the same as, or as similar as possible to, the route of administration of the compound to man for therapeutic purposes.

[0082] When a compound is to be administered by inhalation, special techniques for generating test atmospheres are necessary. The methods usually involve aerosolization or nebulization of fluids containing the compound. If the agent to be tested is a fluid that has an appreciable vapor pressure, it may be administered by passing air through the solution under controlled temperature conditions. Under these conditions, dose is estimated from the volume of air inhaled per unit time, the temperature of the solution, and the vapor pressure of the agent involved. Gases are metered from reservoirs. When particles of a solution are to be administered, unless the particle size is less than about 2  $\mu\text{m}$  the particles will not reach the terminal alveolar sacs in the lungs. A variety of apparatuses and chambers are available to perform studies for detecting effects of irritant or other toxic endpoints when they are administered by inhalation. The preferred method of administering an agent to animals is via the oral route, either by intubation or by incorporating the agent in the feed.

[0083] When the agent is exposed to cells *in vitro* or in cell culture, the cell population to be exposed to the agent may be divided into two or more subpopulations, for instance, by

dividing the population into two or more identical aliquots. In some preferred embodiments of the methods of the invention, the cells to be exposed to the agent are derived from heart tissue. For instance, cultured or freshly isolated rat heart cells may be used.

[0084] The methods of the invention may be used generally to predict at least one toxic response, and, as described in the Examples, may be used to predict the likelihood that a compound or test agent will induce various specific heart pathologies, such as tissue necrosis, myocarditis, arrhythmias, tachycardia, myocardial ischemia, angina, hypertension, hypotension, dyspnea, cardiogenic shock, or other pathologies associated with at least one of the toxins herein described. The methods of the invention may also be used to determine the similarity of a toxic response to one or more individual compounds. In addition, the methods of the invention may be used to predict or elucidate the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin (see Tables 5-5LL).

*Diagnostic Uses for the Toxicity Markers*

[0085] As described above, the genes and gene expression information or portfolios of the genes with their expression information as provided in Tables 1-5LL may be used as diagnostic markers for the prediction or identification of the physiological state of a tissue or cell sample that has been exposed to a compound or to identify or predict the toxic effects of a compound or agent. For instance, a tissue sample such as a sample of peripheral blood cells or some other easily obtainable tissue sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 5-5LL may be compared to the expression levels found in tissues or cells exposed to the toxins described herein. These methods may result in the diagnosis of a physiological state in the cell, may be used to diagnose toxin exposure or may be used to identify the potential toxicity of a compound, for instance a new or unknown compound or agent that the subject has been exposed to. The comparison of expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described below.

[0086] In another format, the levels of a gene(s) of Tables 5-5LL, its encoded protein(s), or any metabolite produced by the encoded protein may be monitored or detected in a sample, such as a bodily tissue or fluid sample to identify or diagnose a physiological state

of an organism. Such samples may include any tissue or fluid sample, including urine, blood and easily obtainable cells such as peripheral lymphocytes.

*Use of the Markers for Monitoring Toxicity Progression*

[0087] As described above, the genes and gene expression information provided in Tables 5-5LL may also be used as markers for the monitoring of toxicity progression, such as that found after initial exposure to a drug, drug candidate, toxin, pollutant, *etc.* For instance, a tissue or cell sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 5-5LL may be compared to the expression levels found in tissue or cells exposed to the cardiotoxins described herein. The comparison of the expression data, as well as available sequence or other information may be done by a researcher or diagnostician or may be done with the aid of a computer and databases.

*Use of the Toxicity Markers for Drug Screening*

[0088] According to the present invention, the genes identified in Tables 1-5LL may be used as markers or drug targets to evaluate the effects of a candidate drug, chemical compound or other agent on a cell or tissue sample. The genes may also be used as drug targets to screen for agents that modulate their expression and/or activity. In various formats, a candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of a drug's effects by looking at the number of markers which the drug induces and comparing them. More specific drugs will have less transcriptional targets. Similar sets of markers identified for two drugs may indicate a similarity of effects.

[0089] Assays to monitor the expression of a marker or markers as defined in Tables 1-5LL may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

[0090] In one assay format, gene chips containing probes to one, two or more genes from Tables 1-5LL may be used to directly monitor or detect changes in gene expression in the treated or exposed cell. Cell lines, tissues or other samples are first exposed to a test agent

and in some instances, a known toxin, and the detected expression levels of one or more, or preferably 2 or more of the genes of Tables 1-5LL are compared to the expression levels of those same genes exposed to a known toxin alone. Compounds that modulate the expression patterns of the known toxin(s) would be expected to modulate potential toxic physiological effects *in vivo*. The genes in Tables 1-5LL are particularly appropriate markers in these assays as they are differentially expressed in cells upon exposure to a known cardiotoxin. Tables 1 and 2 disclose those genes that are differentially expressed upon exposure to the named toxins and their corresponding GenBank Accession numbers. Table 3 discloses the human homologues and the corresponding GenBank Accession numbers of the differentially expressed genes of Tables 1 and 2.

[0091] In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the transcriptional regulatory regions of a gene in Tables 1-5LL and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.* (1990), *Anal Biochem* 188: 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

[0092] Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 5-5LL. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time, and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.* (Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

[0093] In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cells and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector) construct comprising an operable non-translated 5'-

promoter containing end of the structural gene encoding the gene products of Tables 1-5LL fused to one or more antigenic fragments or other detectable markers, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct or other detectable tag. Such a process is well known in the art (see Sambrook *et al.*, *supra*).

[0094] Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells are disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the “agent-contacted” sample is then compared with the control samples (no exposure and exposure to a known toxin) where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the “agent-contacted” sample compared to the control is used to distinguish the effectiveness and/or toxic effects of the agent.

*Use of Toxicity Markers to Identify Agents that Modulate Protein Activity or Levels*

[0095] Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein(s) encoded by the genes in Tables 1-5LL. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

[0096] In one format, the relative amounts of a protein (Tables 1-5LL) between a cell population that has been exposed to the agent to be tested compared to an unexposed control cell population and a cell population exposed to a known toxin may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are



exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

[0097] Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of a protein of the invention alone or with its associated substrates, binding partners, *etc.* An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

[0098] As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

[0099] The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see G.A. Grant in: Molecular Biology and Biotechnology, Meyers, ed., pp. 659-664, VCH Publishers, New York, 1995). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

#### *Nucleic Acid Assay Formats*

[00100] As previously discussed, the genes identified as being differentially expressed upon exposure to a known cardiotoxin (Tables 1-5LL) may be used in a variety of nucleic acid detection assays to detect or quantify the expression level of a gene or multiple genes in a given sample. The genes described in Tables 1-5LL may also be used in combination with one or more additional genes whose differential expression is associate with toxicity in a cell or tissue. In preferred embodiments, the genes in Tables 5-5LL may be combined

with one or more of the genes described in prior and related applications 60/303,819 filed on July 10, 2001; 60/305,623 filed on July 17, 2001; 60/369,351 filed on April 3, 2002; and 60/377,611 filed on May 6, 2002; 09/917,800; 10/060,087; 10/152,319; 10/191,803, and 10/301,856, all of which are incorporated by reference.

**[00101]** Any assay format to detect gene expression may be used. For example, traditional Northern blotting, dot or slot blot, nuclease protection, primer directed amplification, RT-PCR, semi- or quantitative PCR, branched-chain DNA and differential display methods may be used for detecting gene expression levels. Those methods are useful for some embodiments of the invention. In cases where smaller numbers of genes are detected, amplification based assays may be most efficient. Methods and assays of the invention, however, may be most efficiently designed with hybridization-based methods for detecting the expression of a large number of genes.

**[00102]** Any hybridization assay format may be used, including solution-based and solid support-based assay formats. Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, particles, beads, microparticles or silicon or glass based chips, *etc.* Such chips, wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755).

**[00103]** Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000, 400,000 or 1,000,000 or more of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of about a square centimeter. Probes corresponding to the genes of Tables 5-5LL or from the related applications described above may be attached to single or multiple solid support structures, *e.g.*, the probes may be attached to a single chip or to multiple chips to comprise a chip set.

**[00104]** Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart *et al.* (1996), *Nat Biotechnol* 14: 1675-1680; McGall *et al.* (1996), *Proc Nat Acad Sci USA* 93: 13555-

13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described in Tables 5-5LL. For instance, such arrays may contain oligonucleotides that are complementary to or hybridize to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70, 100 or more of the genes described herein. Preferred arrays contain all or nearly all of the genes listed in Tables 1-5LL, or individually, the gene sets of Tables 5-5LL. In a preferred embodiment, arrays are constructed that contain oligonucleotides to detect all or nearly all of the genes in any one of or all of Tables 1-5LL on a single solid support substrate, such as a chip.

**[00105]** The sequences of the expression marker genes of Tables 1-5LL are in the public databases. Table 1 provides the GenBank Accession Number for each of the sequences (see *www.ncbi.nlm.nih.gov/*) as well as a corresponding SEQ ID NO. in the sequence listing filed with this application. Table 3 provides the LocusLink and Unigene names and descriptions for the human homologues of the genes described in Tables 1 and 2. The sequences of the genes in GenBank and/or RefSeq are expressly herein incorporated by reference in their entirety as of the filing date of this application, as are related sequences, for instance, sequences from the same gene of different lengths, variant sequences, polymorphic sequences, genomic sequences of the genes and related sequences from different species, including the human counterparts, where appropriate (see Table 3). These sequences may be used in the methods of the invention or may be used to produce the probes and arrays of the invention. In some embodiments, the genes in Tables 1-5LL that correspond to the genes or fragments previously associated with a toxic response may be excluded from the Tables.

**[00106]** As described above, in addition to the sequences of the GenBank Accession Numbers disclosed in the Tables 1-5LL, sequences such as naturally occurring variants or polymorphic sequences may be used in the methods and compositions of the invention. For instance, expression levels of various allelic or homologous forms of a gene disclosed in Tables 1-5LL may be assayed. Any and all nucleotide variations that do not significantly alter the functional activity of a gene listed in the Tables 1-5LL, including all naturally occurring allelic variants of the genes herein disclosed, may be used in the methods and to make the compositions (*e.g.*, arrays) of the invention.

**[00107]** Probes based on the sequences of the genes described above may be prepared by any commonly available method. Oligonucleotide probes for screening or assaying a tissue or cell sample are preferably of sufficient length to specifically hybridize only to

appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least about 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases, longer probes of at least 30, 40, or 50 nucleotides will be desirable.

**[00108]** As used herein, oligonucleotide sequences that are complementary to one or more of the genes described in Tables 1-5LL refer to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequences of said genes, their encoded RNA or mRNA, or amplified versions of the RNA such as cRNA. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

**[00109]** “Bind(s) substantially” refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

**[00110]** The terms “background” or “background signal intensity” refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (*e.g.*, the oligonucleotide probes, control probes, the array substrate, *etc.*). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (*e.g.* probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

[00111] The phrase “hybridizing specifically to” or “specifically hybridizes” refers to the binding, duplexing, or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA.

[00112] Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 100,000 or 1,000,000 or more different nucleic acid hybridizations.

[00113] As used herein a “probe” is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

[00114] The term “perfect match probe” refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a “test probe”, a “normalization control” probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a “mismatch control” or “mismatch probe.”

[00115] The terms “mismatch control” or “mismatch probe” refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

[00116] While the mismatch(es) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

[00117] The term “stringent conditions” refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength and pH.

[00118] Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M Na<sup>+</sup> ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

[00119] The “percentage of sequence identity” or “sequence identity” is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical submit (*e.g.* nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

#### *Probe design*

[00120] One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of test probes that specifically hybridize to the sequences of interest. Probes may be produced from any region of the genes identified in the Tables and the attached representative sequence listing. In instances where the gene reference in the Tables is an EST, probes may be designed from that sequence or from other regions of the corresponding full-length transcript that may be available in any of the sequence databases, such as those herein described. See WO 99/32660 for methods of producing

probes for a given gene or genes. In addition, any available software may be used to produce specific probe sequences, including, for instance, software available from Molecular Biology Insights, Olympus Optical Co. and Biosoft International. In a preferred embodiment, the array will also include one or more control probes.

[00121] High density array chips of the invention include “test probes.” Test probes may be oligonucleotides that range from about 5 to about 500, or about 7 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 35 nucleotides in length. In other particularly preferred embodiments, the probes are 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences such as cDNA fragments. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using native nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

[00122] In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes may fall into three categories referred to herein as 1) normalization controls; 2) expression level controls; and 3) mismatch controls.

[00123] Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample to be screened. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, “reading” efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (*e.g.*, fluorescence intensity) read from all other probes in the array are divided by the signal (*e.g.*, fluorescence intensity) from the control probes thereby normalizing the measurements.

[00124] Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of

the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (*i.e.*, no secondary structure) and do not match any target-specific probes.

[00125] Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typically expression level control probes have sequences complementary to subsequences of constitutively expressed “housekeeping genes” including, but not limited to the actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

[00126] Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (*e.g.*, stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a 20 mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

[00127] Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation, for instance, a mutation of a gene in the accompanying Tables 1-5LL. The difference in intensity between the perfect match and the mismatch probe provides a good measure of the concentration of the hybridized material.

#### *Nucleic Acid Samples*

[00128] Cell or tissue samples may be exposed to the test agent *in vitro* or *in vivo*. When cultured cells or tissues are used, appropriate mammalian cell extracts, such as liver cell



extracts, may also be added with the test agent to evaluate agents that may require biotransformation to exhibit toxicity.

[00129] The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may or may not be cloned. The genes may or may not be amplified and cRNA produced. The cloning and/or amplification do not appear to bias the representation of genes within a population. In some assays, it may be preferable, however, to use polyA<sup>+</sup> RNA as a source, as it can be used with less processing steps.

[00130] As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24, Hybridization With Nucleic Acid Probes: Theory and Nucleic Acid Probes, P. Tijssen, Ed., Elsevier Press, New York, 1993. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and RNA transcribed from the amplified DNA (cRNA). One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates are used.

[00131] Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a tissue or cell sample that has been exposed to a compound, agent, drug, pharmaceutical composition, potential environmental pollutant or other composition. In some formats, the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to, sputum, blood, blood-cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom. Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

#### *Forming High Density Arrays*

[00132] Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a single or on multiple solid substrates by a variety of methods, including,

but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung, U.S. Patent No. 5,143,854).

[00133] In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

[00134] In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in PCT Publication Nos. WO 93/09668 and WO 01/23614. High density nucleic acid arrays can also be fabricated by depositing pre-made or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

#### *Hybridization*

[00135] Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. See WO 99/32660. The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid duplexes (*e.g.*, DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower

stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization tolerates fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency.

[00136] In a preferred embodiment, hybridization is performed at low stringency, in this case in 6x SSPET at 37°C (0.005% Triton X-100), to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*, 1x SSPET at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25x SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (*e.g.*, expression level control, normalization control, mismatch controls, *etc.*).

[00137] In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

#### *Signal Detection*

[00138] The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. See WO 99/32660.

#### *Databases*

[00139] The present invention includes relational databases, such as the Gene Logic ToxExpress® database, containing sequence information, for instance, for the genes of Tables 1-5LL, as well as gene expression information from tissue or cells exposed to various standard toxins, such as those herein described (see Tables 5-5LL). Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information (see

Tables 1 and 2), or descriptive information concerning the clinical status of the tissue sample, or the animal from which the sample was derived. The database may be designed to include different parts, for instance a sequence database and a gene expression database. Methods for the configuration and construction of such databases and computer-readable media to which such databases are saved are widely available, for instance, see U.S. Patent No. 5,953,727, which is herein incorporated by reference in its entirety.

**[00140]** The databases of the invention may be linked to an outside or external database such as GenBank ([www.ncbi.nlm.nih.gov/entrez/index.html](http://www.ncbi.nlm.nih.gov/entrez/index.html)); KEGG ([www.genome.ad.jp/kegg](http://www.genome.ad.jp/kegg)); SPAD ([www.grt.kyushu-u.ac.jp/spad/index.html](http://www.grt.kyushu-u.ac.jp/spad/index.html)); HUGO ([www.gene.ucl.ac.uk/hugo](http://www.gene.ucl.ac.uk/hugo)); Swiss-Prot ([www.expasy.ch/sprot](http://www.expasy.ch/sprot)); Prosite ([www.expasy.ch/tools/scnpsit1.html](http://www.expasy.ch/tools/scnpsit1.html)); OMIM ([www.ncbi.nlm.nih.gov/omim](http://www.ncbi.nlm.nih.gov/omim)); and GDB ([www.gdb.org](http://www.gdb.org)). In a preferred embodiment, as described in Tables 1-3, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI) ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)).

**[00141]** Any appropriate computer platform, user interface, *etc.* may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or information provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such as those available from Silicon Graphics. Client/server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

**[00142]** The databases of the invention may be used to produce, among other things, ToxScreen™ reports and electronic Northern (E-NORTHERN™, Gene Logic, Inc., Gaithersburg, MD) that allow the user to determine the cell type or tissue in which a given gene is expressed or allow determination of the abundance or expression level of a given gene in a particular tissue or cell, for instance, a cell or tissue sample exposed to a test compound.

**[00143]** The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising one or more of the genes in Tables 5-5LL, comprising the step of comparing the expression level of at least one gene in Tables 5-5LL in a cell or tissue exposed to a test agent to the level of expression of the gene in the database. Such methods may be used to predict the toxic potential of a given compound by comparing the level of expression of a gene or genes in

Tables 5-5LL from a tissue or cell sample exposed to the test agent to the expression levels found in a control tissue or cell samples exposed to a standard toxin or cardiotoxin such as those herein described. Such methods may also be used in the drug or agent screening assays as described herein.

#### *Kits*

**[00144]** The invention further includes kits combining, in different combinations, high-density oligonucleotide arrays, reagents for use with the arrays, protein reagents encoded by the genes of the Tables, signal detection and array-processing instruments, gene expression databases and analysis and database management software described above. The kits may be used, for example, to predict or model the toxic response of a test compound, to monitor the progression of heart disease states, to identify genes that show promise as new drug targets and to screen known and newly designed drugs as discussed above.

**[00145]** The databases packaged with the kits are a compilation of expression patterns from human or laboratory animal genes and gene fragments (corresponding to the genes of Tables 1-5LL). In particular, the database software and packaged information that may contain the databases saved to a computer-readable medium include the expression results of Tables 1-5LL that can be used to predict toxicity of a test agent by comparing the expression levels of the genes of Tables 1-5LL induced by the test agent to the expression levels presented in Tables 5-5LL. In another format, database and software information may be provided in a remote electronic format, such as a website, the address of which may be packaged in the kit.

**[00146]** Databases and software designed for use with microarrays is discussed in PCT/US99/20449, filed September 8, 1999, Genomic Knowledge Discovery, PCT/IB00/00863, filed June 28, 2000, Biological Data Processing, and in Balaban *et al.*, U.S. Patent Nos. 6,229,911, a computer-implemented method for managing information, stored as indexed tables, collected from small or large numbers of microarrays, and 6,185,561, a computer-based method with data mining capability for collecting gene expression level data, adding additional attributes and reformatting the data to produce answers to various queries. Chee *et al.*, U.S. Patent No. 5,974,164, disclose a software-based method for identifying mutations in a nucleic acid sequence based on differences in probe fluorescence intensities between wild type and mutant sequences that hybridize to reference sequences.

[00147] The kits may be used in the pharmaceutical industry, where the need for early drug testing is strong due to the high costs associated with drug development, but where bioinformatics, in particular gene expression informatics, is still lacking. These kits will reduce the costs, time and risks associated with traditional new drug screening using cell cultures and laboratory animals. The results of large-scale drug screening of pre-grouped patient populations, pharmacogenomics testing, can also be applied to select drugs with greater efficacy and fewer side-effects. The kits may also be used by smaller biotechnology companies and research institutes who do not have the facilities for performing such large-scale testing themselves.

[00148] Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

## EXAMPLES

### EXAMPLE 1: IDENTIFICATION OF TOXICITY MARKERS

[00149] The cardiotoxins adriamycin, amphotericin B, epirubicin, phenylpropanolamine, and rosiglitazone were administered to male Sprague-Dawley rats at various time points using administration diluents, protocols, and dosing regimes as indicated in Table 6. The cardiotoxins and control compositions, including cyclophosphamide, ifosfamide, minoxidil, hydralazine, BI-QT, clenbuterol, isoproterenol, norepinephrine, and epinephrine were administered to male Sprague-Dawley rats at various time points using administration diluents, protocols and dosing regimes as previously described in the art and previously described in the priority applications discussed above. The low and high dose level for each compound are provided in the chart below.

Heart Toxin	Low Dose (mg/kg)	High Dose (mg/kg)
Cyclophosphamide	20	200
Ifosfamide	5	100
Minoxidil	12 mg/L	120 mg/L
Hydralazine	2.5	25
BI-QT	10	50
Clenbuterol	0.4	4
Isoproterenol	0.05	0.5
Norepinephrine	0.05	0.5
Epinephrine	0.1	1

Heart Toxin	Low Dose (mg/kg)	High Dose (mg/kg)
Adriamycin	1.3	12.8
Amphotericin B	0.25	2.5
Epirubicin	1.2	12
Phenylpropanolamine	6.4	64
Rosiglitazone	18	180

[00150] After administration, the dosed animals were observed and tissues were collected as described below:

### Observation of Animals

[00151] 1. Clinical Observations- Twice daily: mortality and moribundity check.

Cage Side Observations - skin and fur, eyes and mucous membrane, respiratory system, circulatory system, autonomic and central nervous system, somatomotor pattern, and behavior pattern. Potential signs of toxicity, including tremors, convulsions, salivation, diarrhea, lethargy, coma or other atypical behavior or appearance, were recorded as they occurred and included a time of onset, degree, and duration.

[00152] 2. Physical Examinations- Prior to randomization, prior to initial treatment, and prior to sacrifice.

[00153] 3. Body Weights- Prior to randomization, prior to initial treatment, and prior to sacrifice.

### Clinical Pathology

[00154] 1. Frequency Prior to necropsy.

[00155] 2. Number of animals All surviving animals.

[00156] 3. Bleeding Procedure Blood was obtained by puncture of the orbital sinus while under 70% CO<sub>2</sub>/ 30% O<sub>2</sub> anesthesia.

[00157] 4. Collection of Blood Samples Approximately 0.5 mL of blood was collected into EDTA tubes for evaluation of hematology parameters. Approximately 1 mL of blood was collected into serum separator tubes for clinical chemistry analysis. Approximately 200 µL of plasma was obtained and frozen at ~-80°C for test compound/metabolite estimation. An additional ~2 mL of blood was collected into a 15 mL conical polypropylene vial to which ~3 mL of Trizol was immediately added. The contents were immediately mixed with a vortex and by repeated inversion. The tubes were frozen in liquid nitrogen and stored at ~-80°C.

### Termination Procedures

*Terminal Sacrifice*

[00158] At the sampling times indicated in Tables 5A-5LL and Table 6 for each cardiotoxin, and as previously described in the related applications mentioned above, rats were weighed, physically examined, sacrificed by decapitation, and exsanguinated. The animals were necropsied within approximately five minutes of sacrifice. Separate sterile, disposable instruments were used for each animal, with the exception of bone cutters, which were used to open the skull cap. The bone cutters were dipped in disinfectant solution between animals.

[00159] Necropsies were conducted on each animal following procedures approved by board-certified pathologists.

[00160] Animals not surviving until terminal sacrifice were discarded without necropsy (following euthanasia by carbon dioxide asphyxiation, if moribund). The approximate time of death for moribund or found dead animals was recorded.

*Postmortem Procedures*

[00161] Fresh and sterile disposable instruments were used to collect tissues. Gloves were worn at all times when handling tissues or vials. All tissues were collected and frozen within approximately 5 minutes of the animal's death. The liver sections and kidneys were frozen within approximately 3-5 minutes of the animal's death. The time of euthanasia, an interim time point at freezing of liver sections and kidneys, and time at completion of necropsy were recorded. Tissues were stored at approximately -80°C or preserved in 10% neutral buffered formalin.

*Tissue Collection and Processing*

[00162] Liver-

1. Right medial lobe – snap frozen in liquid nitrogen and stored at ~-80°C.
2. Left medial lobe - Preserved in 10% neutral-buffered formalin (NBF) and evaluated for gross and microscopic pathology.
3. Left lateral lobe – snap frozen in liquid nitrogen and stored at ~-80°C.

[00163] Heart-

A sagittal cross-section containing portions of the two atria and of the two ventricles was preserved in 10% NBF. The remaining heart was frozen in liquid nitrogen and stored at ~-80°C.

[00164] Kidneys (both)-



1. Left – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at  $\sim -80^{\circ}\text{C}$ .
2. Right – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at  $\sim -80^{\circ}\text{C}$ .

**[00165]** Testes (both)-

A sagittal cross-section of each testis was preserved in 10% NBF. The remaining testes were frozen together in liquid nitrogen and stored at  $\sim -80^{\circ}\text{C}$ .

**[00166]** Brain (whole)-

A cross-section of the cerebral hemispheres and of the diencephalon was preserved in 10% NBF, and the rest of the brain was frozen in liquid nitrogen and stored at  $\sim -80^{\circ}\text{C}$ .

**[00167]** Microarray sample preparation was conducted with minor modifications, following the protocols set forth in the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was ground to a powder using a Spex Certiprep 6800 Freezer Mill. Total RNA was extracted with Trizol (GibcoBRL) utilizing the manufacturer's protocol. The total RNA yield for each sample was 200-500  $\mu\text{g}$  per 300 mg tissue weight. mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen) followed by ethanol precipitation. Double stranded cDNA was generated from mRNA using the SuperScript Choice system (GibcoBRL). First strand cDNA synthesis was primed with a T7-(dT24) oligonucleotide. The cDNA was phenol-chloroform extracted and ethanol precipitated to a final concentration of 1  $\mu\text{g}/\text{ml}$ . From 2  $\mu\text{g}$  of cDNA, cRNA was synthesized using Ambion's T7 MegaScript in vitro Transcription Kit.

**[00168]** To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. Following a  $37^{\circ}\text{C}$  incubation for six hours, impurities were removed from the labeled cRNA following the RNeasy Mini kit protocol (Qiagen). cRNA was fragmented (fragmentation buffer consisting of 200 mM Tris-acetate, pH 8.1, 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at  $94^{\circ}\text{C}$ . Following the Affymetrix protocol, 55  $\mu\text{g}$  of fragmented cRNA was hybridized on the Affymetrix rat array set for twenty-four hours at 60 rpm in a  $45^{\circ}\text{C}$  hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Data was analyzed using Affymetrix GeneChip®

version 2.0 and Expression Data Mining (EDMT) software (version 1.0), Gene Logic's GeneExpress® 2000 software and S-Plus™ software.

[00169] Tables 1 and 2 disclose those genes that are differentially expressed upon exposure to the named toxins and their corresponding GenBank Accession and Sequence Identification numbers, the identities of the metabolic pathways in which the genes function, the gene names if known, and the Unigene Cluster titles. The human homologues of the rat genes in Tables 1 and 2 are indicated in Table 3. The model codes in Tables 1-3 represent the various toxicity or heart pathology states that differential expression of each gene is able to identify, as well as the individual toxin or toxin type associated with differential expression of each gene. The model codes are defined in Table 4. The GLGC ID is the internal Gene Logic identification number.

[00170] Tables 5A-5LL disclose a set of genes, along with the summary statistics for each of the comparisons performed as indicated in these tables, *i.e.*, expression levels of a particular gene in toxicity group samples compared to non-toxicity group samples in response to exposure to a particular toxin, or as measured in a particular disease state. Each of these tables contains a set of predictive genes and creates a model for predicting the cardiotoxicity of an unknown, *i.e.*, untested compound. Each gene is identified by its Gene Logic identification number and can be cross-referenced to a gene name and representative sequence identification number in Tables 1 and 2 or in one or more related applications, as mentioned on page 1.

[00171] For each comparison of gene expression levels between samples in the toxicity group (samples affected by exposure to a specific toxin) and samples in the non-toxicity group (samples not affected by exposure to that same specific toxin), the tox mean (for toxicity group samples) is the mean signal intensity, as normalized for the various chip parameters that are being assayed. The non-tox mean represents the mean signal intensity, as normalized for the various chip parameters that are being assayed, in samples from animals other than those treated with the high dose of the specific toxin. These animals were treated with a low dose of the specific toxin, or with vehicle alone, or with a different toxin. Samples in the toxicity groups were obtained from animals sacrificed at the time point(s) indicated in the Table 5-5LL headings, while samples in the non-toxicity groups were obtained from animals sacrificed at all time points in the experiments. For individual genes, an increase in the tox mean compared to the non-tox mean indicates up-regulation

upon exposure to a toxin. Conversely, a decrease in the tox mean compared to the non-tox mean indicates down-regulation.

[00172] The mean values are derived from Average Difference (AveDiff) values for a particular gene, averaged across the corresponding samples. Each individual Average Difference value is calculated by integrating the intensity information from multiple probe pairs that are tiled for a particular fragment. The normalization multiplies each expression intensity for a given experiment (chip) by a global scaling factor. The intent of this normalization is to make comparisons of individual genes between chips possible. The scaling factor is calculated as follows:

[00173] 1. From all the unnormalized expression values in the experiment, delete the largest 2% and smallest 2% of the values. That is, if the experiment yields 10,000 expression values, order the values and delete the smallest 200 and largest 200.

[00174] 2. Compute the trimmed mean, which is equal to the mean of the remaining values.

[00175] 3. Compute the scale factor  $SF = 100/(\text{trimmed mean})$

[00176] Values greater than  $2.0 * SD$  noise are assumed to come from expressers. For these values, the standard deviation  $SD \log(\text{signal})$  of the logarithms is calculated. The logarithms are then multiplied by a scale factor proportional to  $1/SD \log(\text{signal})$  and exponentiated. The resulting values are then multiplied by another scale factor, chosen so there will be no discontinuity in the normalized values from unscaled values on either side of  $2.0 * SD$  noise. Some AveDiff values may be negative due to the general noise involved in nucleic acid hybridization experiments. Although many conclusions can be made corresponding to a negative value on the GeneChip platform, it is difficult to assess the meaning behind the negative value for individual fragments. Our observations show that, although negative values are observed at times within the predictive gene set, these values reflect a real biological phenomenon that is highly reproducible across all the samples from which the measurement was taken. For this reason, those genes that exhibit a negative value are included in the predictive set. It should be noted that other platforms of gene expression measurement may be able to resolve the negative numbers for the corresponding genes. The predictive ability of each of those genes should extend across platforms, however. Each mean value is accompanied by the standard deviation for the mean. The linear discriminant analysis score (discriminant score, or LDA), as disclosed in

the tables, measures the ability of each gene to predict whether or not a sample is toxic. The discriminant score is calculated by the following steps:

*Calculation of a discriminant score*

[00177] Let  $X_i$  represent the AveDiff values for a given gene across the non-tox samples,  $i=1\dots n$ .

[00178] Let  $Y_i$  represent the AveDiff values for a given gene across the tox samples,  $i=1\dots t$ .

[00179] The calculations proceed as follows:

[00180] 1. Calculate mean and standard deviation for  $X_i$ 's and  $Y_i$ 's, and denote these by  $m_X, m_Y, s_X, s_Y$ .

[00181] 2. For all  $X_i$ 's and  $Y_i$ 's, evaluate the function  $f(z) = ((1/s_Y) * \exp(-0.5 * ((z - m_Y)/s_Y)^2)) / (((1/s_Y) * \exp(-0.5 * ((z - m_Y)/s_Y)^2)) + ((1/s_X) * \exp(-0.5 * ((z - m_X)/s_X)^2)))$ .

[00182] 3. The number of correct predictions, say  $P$ , is then the number of  $Y_i$ 's such that  $f(Y_i) > 0.5$  plus the number of  $X_i$ 's such that  $f(X_i) < 0.5$ .

[00183] 4. The discriminant score is then  $P/(n+t)$ .

[00184] Linear discriminant analysis uses both the individual measurements of each gene and the calculated measurements of all combinations of genes to classify samples. For each gene a weight is derived from the mean and standard deviation of the toxic and nontox groups. Every gene is multiplied by a weight and the sum of these values results in a collective discriminate score. This discriminant score is then compared against collective centroids of the tox and nontox groups. These centroids are the average of all tox and nontox samples respectively. Therefore, each gene contributes to the overall prediction. This contribution is dependent on weights that are large positive or negative numbers if the relative distances between the tox and nontox samples for that gene are large and small numbers if the relative distances are small. The discriminant score for each unknown sample and centroid values can be used to calculate a probability between zero and one as to the group in which the unknown sample belongs.

## **EXAMPLE 2: GENERAL TOXICITY MODELING**

[00185] Samples were selected for grouping into tox-responding and non-tox-responding groups by examining each study individually with Principal Components Analysis (PCA) to determine which treatments had an observable response. Only groups where confidence

of their tox-responding and non-tox-responding status was established were included in building a general tox model (Tables 5A-5LL).

[00186] Linear discriminant models were generated to describe toxic and non-toxic samples. The top discriminant genes and/or EST's were used to determine toxicity by calculating each gene's contribution with homo and heteroscedastic treatment of variance and inclusion or exclusion of mutual information between genes. Prediction of samples within the database exceeded 80% true positives with a false positive rate of less than 5%. It was determined that combinations of genes and/or EST's generally provided a better predictive ability than individual genes and that the more genes and/or EST used the better predictive ability. Although the preferred embodiment includes fifty or more genes, many pairings or greater combinations of genes and/or EST can work better than individual genes. All combinations of two or more genes from the selected list (Tables 5A-5LL) could be used to predict toxicity. These combinations could be selected by pairing in an agglomerate, divisive, or random approach. Further, as yet undetermined genes and/or EST's could be combined with individual or combination of genes and/or EST's described here to increase predictive ability. However, the genes and/or EST's described here would contribute most of the predictive ability of any such undetermined combinations.

[00187] Other variations on the above method can provide adequate predictive ability. These include selective inclusion of components via agglomerate, divisive, or random approaches or extraction of loading and combining them in agglomerate, divisive, or random approaches. Also the use of composite variables in logistic regression to determine classification of samples can also be accomplished with linear discriminate analysis, neural or Bayesian networks, or other forms of regression and classification based on categorical or continual dependent and independent variables.

### **EXAMPLE 3: MODELING WITH CORE GENE SET**

[00188] As described in Examples 1 and 2, above, the data collected from microarray hybridization experiments were analyzed by LDA and by PCA. The genes in Tables 5G, 5I, 5K, 5M, 5O, 5Q, 5T, 5V, 5X, 5Z, 5BB, 5DD, 5FF, and 5KK constitute a core set of markers for predicting the cardiotoxicity of a compound, whereas the genes in Tables 5H, 5J, 5L, 5N, 5P, 5S, 5U, 5W, 5Y, 5AA, 5CC and 5EE constitute an alternative set of markers. The core marker tables comprise genes that are also found in PCT Application No. PCT/US02/21735, whereas the alternate marker tables do not comprise genes also found in the '735 application. Each gene fragment in Tables 1-5LL is assigned an LDA

score, and those gene fragments in the core set are those with the highest LDA scores. The gene fragments in Tables 5A-5LL were determined to give greater than 80% true positive results and less than 5% false positive results. Gene expression profiles prepared or obtained from expression data for these genes, in the presence and absence of toxin treatment, can be used as controls in assays of compounds whose toxic properties have not been examined. Comparison of data from test compound-exposed and test compound-unexposed animals with the data in Tables 5A-5LL allows the prediction of toxic effects- or no toxic effects- upon exposure to the test compound. Thus, the marker gene sets can be used to examine the biological effects of a compound whose toxic properties following exposure are not known and to predict the toxicity in cardiac tissue of this compound.

#### **EXAMPLE 4: MODELING METHODS**

[00189] The above modeling methods provide broad approaches of combining the expression of genes to predict sample toxicity. One could also provide no weight in a simple voting method or determine weights in a supervised or unsupervised method using agglomerate, divisive, or random approaches. All or selected combinations of genes may be combined in ordered, agglomerate, or divisive, supervised or unsupervised clustering algorithms with unknown samples for classification. Any form of correlation matrix may also be used to classify unknown samples. The spread of the group distribution and discriminate score alone provide enough information to enable a skilled person to generate all of the above types of models with accuracy that can exceed discriminate ability of individual genes. Some examples of methods that could be used individually or in combination after transformation of data types include but are not limited to: Discriminant Analysis, Multiple Discriminant Analysis, robust multi-array average (RMA) analysis, partial least squares (PLS) analysis, logistic regression, multiple regression analysis, linear regression analysis, conjoint analysis, canonical correlation, hierarchical cluster analysis, k-means cluster analysis, self-organizing maps, multidimensional scaling, structural equation modeling, support vector machine determined boundaries, factor analysis, neural networks, bayesian classifications, and resampling methods.

#### **EXAMPLE 5: INDIVIDUAL COMPOUND MARKERS**

[00190] Samples were grouped into individual pathology classes based on known toxicological responses and observed clinical chemical and pathology measurements or into early and late phases of observable toxicity within a compound (Tables 1-5LL). The

top 10, 25, 50, 100 genes based on individual discriminate scores were used in a model to ensure that combination of genes provided a better prediction than individual genes. As described above, all combinations of two or more genes from this list could potentially provide better prediction than individual genes when selected in any order or by ordered, agglomerate, divisive, or random approaches. In addition, combining these genes with other genes could provide better predictive ability, but most of this predictive ability would come from the genes listed herein.

**[00191]** Samples may be considered toxic if they score positive in any individual compound represented here or in any modeling method mentioned under general toxicology models based on combination of individual time and dose grouping of individual toxic compounds obtainable from the data. Most logical groupings with one or more genes and one or more sample dose and time points should produce better predictions of general toxicity or similarity to known toxicant than individual genes.

**[00192]** Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, patent applications and publications referred to in this application are herein incorporated by reference in their entirety.

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
13	25120	A03913	f		
14	6917	AA012709	b		ESTs, Highly similar to splicing factor 3b, subunit 1, 155 kDa [Mus musculus] [M.musculus]
15	25098	AA108277	e		
16	25103	AA685876	cc,dd		
17	25104	AA685903	d,e,r		ESTs, Weakly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
18	14580	AA686870	jj,kk		ESTs
19	19222	AA799279	f,g		ESTs, Highly similar to mitochondrial carrier homolog 2 [Mus musculus] [M.musculus]
20	18272	AA799294	e		ESTs
21	22646	AA799301	d		ESTs, Highly similar to LIGA_MOUSE Ligatin [M.musculus]
22	21997	AA799325	jj,kk		ESTs
23	18396	AA799330	a,p,q,y		ESTs, Weakly similar to T47122 cell division protein pelota [imported] - fruit fly (Drosophila melanogaster) [D.melanogaster]
24	15082	AA799396	p,q		ESTs
24	15083	AA799396	b,p,q		ESTs
25	15084	AA799397	b,l,m		ESTs
26	6581	AA799412	e		ESTs, Weakly similar to I67424 hERR-2 homolog - rat (fragment) [R.norvegicus]
27	20042	AA799420	h,l		ESTs
28	2882	AA799423	ll	nexilin	nexilin
29	17137	AA799438	ee,ff,jj,kk		ESTs, Weakly similar to S68418 protein phosphatase 1M chain M110 isoform - rat (fragment) [R.norvegicus]
30	18365	AA799442	cc,dd,gg		ESTs
31	18160	AA799448	e		ESTs
32	18706	AA799471	d		ESTs, Highly similar to TELT_MOUSE Telethonin (Titin cap protein) [M.musculus]
33	23294	AA799472	b		ESTs, Moderately similar to AD16_HUMAN Protein AD-016 (Protein CGI-116) (x0009) [H.sapiens]
34	11350	AA799488	cc,dd,ll		ESTs
35	8289	AA799494	e		ESTs, Highly similar to T46500 hypothetical protein DKFZp434D098.1 - human (fragment) [H.sapiens]
36	18290	AA799497	hh		ESTs
37	17612	AA799511	ll		ESTs, Weakly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
38	15303	AA799518	w,x		ESTs, Highly similar to hypothetical protein FLJ13725; KIAA1930 protein [Homo sapiens] [H.sapiens]
39	16942	AA799520	e		ESTs, Highly similar to ITMB_MOUSE Integral membrane protein 2B (E25B protein) [M.musculus]
40	21120	AA799526	p,q,gg		ESTs, Highly similar to RIKEN cDNA 1700043E15 [Mus musculus] [M.musculus]
41	17687	AA799531	g		ESTs, Weakly similar to M18.3.p [Caenorhabditis elegans] [C.elegans]
41	17688	AA799531	f,g		ESTs, Weakly similar to M18.3.p [Caenorhabditis elegans] [C.elegans]
42	15560	AA799538	s,t		ESTs, Highly similar to SFR2_MOUSE Splicing factor, arginine/serine-rich 2 (Splicing factor SC35) (SC-35) (Splicing component, 35 kDa) (PR264 protein) [M.musculus]



TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
43	17599	AA799539	c		ESTs, Weakly similar to KEAP_RAT Kelch-like ECH associated protein 1 (Cytosolic inhibitor of Nrf2) (lNrf2) [R.norvegicus]
44	24628	AA799542	ii		ESTs
45	11353	AA799569	d		ESTs
46	17212	AA799571	ll		Rattus norvegicus mRNA for ribosomal protein L35
47	20971	AA799576	c		ESTs, Highly similar to T46259 hypothetical protein DKFZp761E0323.1 - human (fragment) [H.sapiens]
48	20972	AA799580	r,jj,kk		ESTs
49	17712	AA799598	f,g		ESTs
50	20975	AA799599	cc,dd		ESTs
51	15844	AA799600	ii		ESTs, Highly similar to hypothetical protein DKFZp586I021 [Homo sapiens] [H.sapiens]
52	13926	AA799601	ll		ESTs
53	16696	AA799607	h,l		ESTs
54	17380	AA799612	w,x	ubiquitin conjugating enzyme	ubiquitin conjugating enzyme
55	18333	AA799614	e		ESTs, Moderately similar to sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae) [Rattus norvegicus] [R.norvegicus]
56	20980	AA799633	l,m		ESTs, Moderately similar to hypothetical protein MGC13016 [Homo sapiens] [H.sapiens]
57	20981	AA799636	y		ESTs
58	20092	AA799637	r,ll		ESTs, Weakly similar to A55071 hydrogen peroxide-inducible protein hic-5 - mouse [M.musculus]
59	18226	AA799641	l		ESTs, Moderately similar to I53063 testicular tumor overexpressed protein - mouse [M.musculus]
60	20982	AA799657	d,e,ii		ESTs, Weakly similar to S68418 protein phosphatase 1M chain M110 isoform - rat (fragment) [R.norvegicus]
61	17759	AA799663	c,hh		ESTs, Highly similar to S37488 gene T10 protein - mouse [M.musculus]
61	17760	AA799663	c		ESTs, Highly similar to S37488 gene T10 protein - mouse [M.musculus]
62	20994	AA799717	cc,dd		ESTs, Highly similar to RPB9_HUMAN DNA-directed RNA polymerase II 14.5 kDa polypeptide (RPB9) (RPB14.5) [H.sapiens]
63	14250	AA799729	j,k	Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)	ESTs, Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
64	18061	AA799735	r	RuvB-like protein 1	RuvB-like protein 1
65	18349	AA799744	j,p,q,y,z		ESTs
66	17494	AA799751	w,x		ESTs
67	17875	AA799755	cc,dd		ESTs, Weakly similar to carboxypeptidase E [Rattus norvegicus] [R.norvegicus]
68	4133	AA799762	e,p,q,ii		ESTs
69	20997	AA799764	hh		ESTs
70	18360	AA799771	u,jj,kk		ESTs
71	11530	AA799773	a,o,q,y,ee,ff,hh,jj,kk		ESTs, Weakly similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]
71	11531	AA799773	a,o,q,z,ff,hh,kk		ESTs, Weakly similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]
72	6425	AA799784	f,aa,bb		ESTs
73	13683	AA799788	e	HHs:cell division cycle 34	ESTs, Moderately similar to I54552 hypothetical serine proteinase - rat [R.norvegicus]

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
74	20998	AA799803	b,l,m		ESTs, Weakly similar to JC6554 complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat [R.norvegicus]
75	14504	AA799804	f,g,cc,dd		ESTs
76	11422	AA799812	a,ee,ff,jj,kk		ESTs, Moderately similar to PTN3_HUMAN Protein tyrosine phosphatase, non-receptor type 3 (Protein-tyrosine phosphatase H1) (PTP-H1) [H.sapiens]
76	11423	AA799812	a,jj,kk,ll		ESTs, Moderately similar to PTN3_HUMAN Protein tyrosine phosphatase, non-receptor type 3 (Protein-tyrosine phosphatase H1) (PTP-H1) [H.sapiens]
77	21000	AA799816	h,l		ESTs, Highly similar to T46306 hypothetical protein DKFZp434D2411.1 - human (fragment) [H.sapiens]
78	21002	AA799832	gg		ESTs
79	21007	AA799861	d		ESTs, Highly similar to IRF7_MOUSE Interferon regulatory factor 7 (IRF-7) [M.musculus]
80	18378	AA799888	hh		ESTs, Highly similar to nuclear localization signal protein absent in velo-cardio-facial patients [Mus musculus] [M.musculus]
81	15011	AA799893	hh		ESTs, Highly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
82	21027	AA799964	h		ESTs
83	18400	AA799991	aa,bb		ESTs
84	18881	AA799992	c,h,l,n,o,w,x		ESTs, Moderately similar to predicted gene ICRFP703B1614Q5.6; ICRFP703N2430Q5.6; C11orf17 [Mus musculus] [M.musculus]
84	18883	AA799992	c,n,o,kk		ESTs, ESTs, Moderately similar to predicted gene ICRFP703B1614Q5.6; ICRFP703N2430Q5.6; C11orf17 [Mus musculus] [M.musculus]
85	16712	AA800015	e	integrin-linked kinase	integrin-linked kinase
86	23343	AA800016	cc,dd		ESTs, Weakly similar to Yeast ABD1 protein like [Caenorhabditis elegans] [C.elegans]
87	23344	AA800034	s,t		ESTs
88	11352	AA800036	f,jj,kk,ll		ESTs
89	19177	AA800062	ll		ESTs
90	13568	AA800169	h,l		ESTs
91	21065	AA800179	s,t		ESTs, Highly similar to NOC4_MOUSE Neighbor of COX4 [M.musculus]
92	4832	AA800190	a,e,ii,kk	HHs:phosphorylase, glycogen; brain	ESTs, Highly similar to S37300 glycogen phosphorylase (EC 2.4.1.1), brain - rat [R.norvegicus]
93	16420	AA800191	f,g		ESTs
94	18430	AA800197	gg		ESTs
95	21069	AA800200	l,m,ee,ff,jj,kk		ESTs
96	21656	AA800202	s,t		ESTs
97	3692	AA800210	hh,jj,kk		ESTs
98	600	AA800222	g,bb		ESTs
99	4130	AA800298	c,g,kk		ESTs
100	21086	AA800305	cc,dd		ESTs, Moderately similar to RB5A_HUMAN Ras-related protein Rab-5A [H.sapiens]
101	24228	AA800318	b,m		ESTs, Moderately similar to IC1_MOUSE Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh) [M.musculus]
102	12253	AA800549	r,ii		ESTs
103	6892	AA800551	e,ee,ff,ii	DnaJ-like protein	DnaJ-like protein
104	13930	AA800613	j,k,p,q,y,z		EST
105	4843	AA800651	f,g		ESTs

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
106	17997	AA800671	u		ESTs, Moderately similar to A54854 Ras GTPase activating protein-related protein - human [H.sapiens]
107	5257	AA800673	s		ESTs, Highly similar to KIAA0164 gene product [Homo sapiens] [H.sapiens]
108	23368	AA800678	a,j,k,jj,kk		ESTs
109	21377	AA800719	w,x		ESTs
110	17648	AA800735	cc,dd		ESTs, Weakly similar to VIL1_MOUSE Villin 1 [M.musculus]
110	17649	AA800735	cc,dd		ESTs, Weakly similar to VIL1_MOUSE Villin 1 [M.musculus]
111	8137	AA800749	g		ESTs
112	19101	AA800787	aa,bb,ll		ESTs
113	12797	AA800790	p,q		ESTs
114	22386	AA800844	g		ESTs, Moderately similar to LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus]
115	17658	AA800853	d,j,k,s,t		ESTs
116	10320	AA800855	b,l,m		ESTs, ESTs, Highly similar to MLF2_MOUSE Myeloid leukemia factor 2 (Myelodysplasia-myeloid leukemia factor 2) [M.musculus]
117	15213	AA800908	hh		ESTs
118	21416	AA800962	hh		ESTs, Highly similar to S11661 talin - mouse [M.musculus]
119	11901	AA801058	d	aldehyde dehydrogenase family 9, subfamily A1	aldehyde dehydrogenase family 9, subfamily A1
120	12086	AA801116	a		ESTs
121	16852	AA801130	h,l	growth factor receptor bound protein 2	growth factor receptor bound protein 2
122	23115	AA801165	c	Testis-specific histone 2a	Testis-specific histone 2a
123	21427	AA801181	cc,dd		ESTs, Highly similar to P52K_HUMAN 52 kDa repressor of the inhibitor of the protein kinase (p58IPK-interacting protein) (58 kDa interferon-induced protein kinase-interacting protein) (P52rIPK) (Death associated protein 4) [H.sapiens]
124	22318	AA801187	h,l		ESTs
125	10549	AA801255	r,kk		ESTs
126	12399	AA801307	gg,ll		ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.sapiens]
127	16388	AA801310	e		ESTs
128	11166	AA801346	n,o		ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus]
129	11995	AA801352	n,o		ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.sapiens]
130	24237	AA817726	kk		ESTs
131	18796	AA817761	e		ESTs
132	23725	AA817816	a		ESTs
133	23828	AA817823	ii	HHs:UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	ESTs, Weakly similar to glycoprotein galactosyltransferase beta 1, 4; beta-1,4-GalT; galactosyltransferase 2 beta 1, 4; B-1,4-GalT1; beta-1,4-GalT1 [Mus musculus] [M.musculus]
134	1754	AA817837	kk	potassium channel, subfamily K, member 2	potassium channel, subfamily K, member 2
135	1802	AA817841	e,bb		ESTs
136	1901	AA817849	n,o		ESTs
137	1998	AA817864	e		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
138	14101	AA817867	ii		ESTs, Highly similar to I48253 beta-N-acetylhexosaminidase (EC 3.2.1.52) alpha chain precursor - mouse [M.musculus]
139	2143	AA817892	r	guanine nucleotide binding protein beta 2 subunit	guanine nucleotide binding protein beta 2 subunit
140	6550	AA817947	d,jj,kk		ESTs
141	5982	AA817999	r		ESTs
142	5996	AA818065	ii		ESTs
143	16756	AA818089	ll	HHs:glycyl-tRNA synthetase	ESTs, Highly similar to SYG_HUMAN Glycyl-tRNA synthetase (Glycine-tRNA ligase) (GlyRS) [H.sapiens]
144	6014	AA818153	ii		ESTs
145	6015	AA818158	l		ESTs
146	6522	AA818261	r		ESTs, Moderately similar to A47318 RNA-binding protein Raly - mouse [M.musculus]
147	6037	AA818288	ll		ESTs
148	367	AA818342	hh		ESTs
149	8058	AA818475	n,o,w,x		ESTs, Highly similar to RIKEN cDNA 2310008M10 [Mus musculus] [M.musculus]
150	6226	AA818521	ll		ESTs
151	8728	AA818615	h,l		ESTs
152	6053	AA818655	t		EST
153	6054	AA818658	p,q,ee,ff	Diphtheria toxin receptor (heparin binding epidermal growth factor - like growth factor)	Diphtheria toxin receptor (heparin binding epidermal growth factor - like growth factor)
154	11864	AA818717	w,x		ESTs
155	4330	AA818747	r,bb,ll		ESTs
156	19723	AA818761	p,q		ESTs
157	6829	AA818784	ii		ESTs
158	4491	AA818798	w,x		Rattus norvegicus mRNA for cathepsin Y, partial cds
159	6073	AA818818	c		EST
160	12690	AA818820	ii		ESTs
161	13428	AA818861	jj,kk		ESTs
162	6092	AA818897	b		ESTs
163	19729	AA818910	d		ESTs
164	6094	AA818911	t		ESTs
165	6098	AA818935	n,o		ESTs
166	6136	AA819086	cc,dd		ESTs
167	5863	AA819111	jj,kk		ESTs
168	12305	AA819220	aa,bb		ESTs
169	9083	AA819332	j,k		ESTs
170	9310	AA819367	cc,dd		ESTs
171	6281	AA819517	hh		ESTs, Weakly similar to JC5707 HYA22 protein - human [H.sapiens]
172	6282	AA819523	bb		ESTs
173	6168	AA819606	aa,bb		
174	6176	AA819657	v		EST
175	16971	AA819691	n,o	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
176	11021	AA819767	p,q		ESTs
177	19451	AA819788	c		ESTs, Weakly similar to 28kD interferon alpha responsive protein [Mus musculus] [M.musculus]
178	18427	AA819891	gg		ESTs, Weakly similar to B36579 inositol 1,4,5-triphosphate receptor 2 - rat [R.norvegicus]

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
179	320	AA819905	hh	stearoyl-Coenzyme A desaturase 1	stearoyl-Coenzyme A desaturase 1
180	9815	AA848218	p,q		ESTs
181	17614	AA848306	b		ESTs, Weakly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
182	23521	AA848407	h,l		ESTs
183	11160	AA848470	ii		ESTs
184	2324	AA848545	r		ESTs, Weakly similar to T19253 hypothetical protein C14A4.11 - Caenorhabditis elegans [C.elegans]
185	25110	AA848546	cc,dd		ESTs, Weakly similar to T19253 hypothetical protein C14A4.11 - Caenorhabditis elegans [C.elegans]
186	14654	AA848795	jj,kk		ESTs
187	7749	AA848804	kk		ESTs, Highly similar to BTF3_MOUSE Transcription factor BTF3 (RNA polymerase B transcription factor 3) [M.musculus]
188	14604	AA848828	c		ESTs
189	12102	AA848902	ii		ESTs, Weakly similar to S12207 hypothetical protein (B2 element) - mouse [M.musculus]
190	18673	AA849028	t	proteasome (prosome, macropain) subunit, alpha type 3	proteasome (prosome, macropain) subunit, alpha type 3
191	8619	AA849317	jj,kk		ESTs
192	2075	AA849394	u,v		ESTs, Weakly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
193	18909	AA849426	h,l		ESTs, Weakly similar to YLC4_CAEEL Hypothetical 81.0 kDa protein C35D10.4 in chromosome III [C.elegans]
194	11726	AA849518	t		ESTs
194	11727	AA849518	t		ESTs
195	21264	AA849731	cc,dd		ESTs
196	24128	AA849766	bb		ESTs, Highly similar to T08750 hypothetical protein DKFZp586E1519.1 - human (fragment) [H.sapiens]
197	21275	AA849796	d		ESTs
198	8515	AA849917	b,v		ESTs
199	11355	AA849957	ll		ESTs
200	22026	AA850060	n,o		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
200	22028	AA850060	cc,dd		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
201	21353	AA850247	d		ESTs
202	19071	AA850524	k		ESTs, Highly similar to I49257 NF2d9 - mouse [M.musculus]
203	6649	AA850563	aa,bb		ESTs
204	19545	AA850735	e		ESTs
205	5668	AA850743	jj,kk		ESTs
206	21754	AA850824	ii		ESTs
207	21761	AA850872	h,l		ESTs
208	21766	AA850916	kk		ESTs
1	19424	AA850922	h,l	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	dimethylarginine dimethylaminohydrolase 1
209	21782	AA851034	u,v		ESTs
210	4490	AA851184	n,o		Rattus norvegicus mRNA for cathepsin Y, partial cds

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
211	4163	AA851210	gg		ESTs, Weakly similar to T33304 hypothetical protein R01B10.5 - <i>Caenorhabditis elegans</i> [C.elegans]
212	21456	AA851239	cc,dd		ESTs, Moderately similar to exostoses (multiple)-like 2; Exostoses, multiple, like 2 [Homo sapiens] [H.sapiens]
213	21465	AA851273	h,l		ESTs, Weakly similar to retinoic acid receptor responder (tazarotene induced) 2 [Homo sapiens] [H.sapiens]
214	19214	AA851364	u,v		ESTs
215	16934	AA851403	b		ESTs, Highly similar to RIKEN cDNA 2900010I05 [Mus musculus] [M.musculus]
216	13627	AA851493	aa,bb	claudin 7	claudin 7
217	21713	AA851637	e,r	Lutheran blood group (Auberger b antigen included)	Lutheran blood group (Auberger b antigen included)
218	21514	AA851660	ee,ff		ESTs
219	19136	AA851788	e		ESTs
220	12187	AA851820	e		ESTs
221	19159	AA851953	u,v		ESTs, Moderately similar to T12501 hypothetical protein DKFZp434O171.1 - human (fragment) [H.sapiens]
222	15260	AA858518	f,g		ESTs, Weakly similar to T51146 ring-box protein 1 [imported] - human [H.sapiens]
223	15283	AA858548	a,kk		ESTs
224	23069	AA858572	u,v		ESTs
225	1801	AA858636	n,o		ESTs, Highly similar to mini chromosome maintenance deficient 7 ( <i>S. cerevisiae</i> ) [Mus musculus] [M.musculus]
226	18350	AA858674	p,q,ee,ff		ESTs
227	12829	AA858695	gg		ESTs, Moderately similar to mitochondrial ribosomal protein S33; mitochondrial 28S ribosomal protein S33 [Homo sapiens] [H.sapiens]
228	13802	AA858853	b,l,m		ESTs, Weakly similar to NTC1_RAT Neurogenic locus notch homolog protein 1 precursor (Notch 1) [R.norvegicus]
229	17236	AA858903	s,t,gg	Tissue inhibitor of metalloproteinase 3	Tissue inhibitor of metalloproteinase 3
230	5867	AA858953	kk		ESTs, Moderately similar to SYN_HUMAN Asparaginyl-tRNA synthetase, cytoplasmic (Asparagine-tRNA ligase) (AsnRS) [H.sapiens]
231	14209	AA858955	j,k		EST
232	17361	AA859114	kk		ESTs
233	6158	AA859284	f,g	procollagen, type I, alpha 2	procollagen, type I, alpha 2
234	6458	AA859319	b,l,m		ESTs
235	15157	AA859343	j,k		ESTs
236	15160	AA859346	u,v		ESTs, Moderately similar to RP38_HUMAN Ribonuclease P protein subunit p38 (RNaseP protein p38) [H.sapiens]
237	16314	AA859348	p,q		ESTs
238	22605	AA859447	q		ESTs
239	23142	AA859479	f		ESTs
240	13595	AA859508	b,s		ESTs
241	23340	AA859519	d,h,l		ESTs, Highly similar to JC6127 RNA-binding protein type 1 - human [H.sapiens]
242	15150	AA859562	d,hh		ESTs
243	4809	AA859616	gg		ESTs, Weakly similar to FYVE zinc finger [Caenorhabditis elegans] [C.elegans]
244	16228	AA859643	c		ESTs
245	11635	AA859645	j,k,ll	attractin	attractin

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
246	16318	AA859648	p,q		ESTs, Weakly similar to DJA1_MOUSE DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) [R.norvegicus]
247	22406	AA859680	y,z		ESTs
247	22407	AA859680	s,t		ESTs
248	20582	AA859688	w,hh		ESTs, Highly similar to AU RNA-binding enoyl-coenzyme A hydratase; AU RNA-binding protein/enoyl-coenzyme A hydratase [Mus musculus] [M.musculus]
249	21440	AA859719	l,m		ESTs
250	22670	AA859750	y,z,hh		ESTs, Weakly similar to ERF_MOUSE ETS-domain transcription factor ERF [M.musculus]
251	2262	AA859757	hh	collagen, type V, alpha 1	collagen, type V, alpha 1
252	22385	AA859805	g,s,t		ESTs, Moderately similar to LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus]
253	14213	AA859827	a,y,z,ee,ff		ESTs, Moderately similar to URK1_MOUSE URIDINE KINASE (URIDINE MONOPHOSPHOKINASE) [M.musculus]
254	22630	AA859848	gg		ESTs
255	22739	AA859877	h,l,ll		ESTs
256	22773	AA859885	c,r,bb		ESTs
257	15165	AA859919	ii		ESTs
257	15166	AA859919	hh		ESTs
258	22940	AA859922	n,o		ESTs
259	18468	AA859966	l,m		ESTs, Moderately similar to TNP1_HUMAN Tumor necrosis factor, alpha-induced protein 1, endothelial (B12 protein) [H.sapiens]
260	23336	AA859981	ee,ff,jj,kk	HHs:inositol(myo)-1(or 4)-monophosphatase 2	ESTs, Weakly similar to MYOP_RAT Myo-inositol-1(or 4)-monophosphatase (IMPase) (IMP) (Inositol monophosphatase) (Lithium-sensitive myo-inositol monophosphatase A1) [R.norvegicus]
261	14206	AA859994	a		ESTs
262	23347	AA860015	aa,bb		ESTs, Weakly similar to T50607 hypothetical protein DKFZp434I016.1 - human (fragment) [H.sapiens]
263	4222	AA860024	h,l,w,x		ESTs, Highly similar to EF1G_MOUSE Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) [M.musculus]
264	23585	AA860029	aa		ESTs
265	13974	AA860030	n,o,w,x,ll		Rattus norvegicus mRNA for class I beta-tubulin, complete cds
266	15846	AA866250	b,l,m		ESTs
267	15884	AA866276	d,f,g,r		ESTs, Weakly similar to A60543 protein kinase (EC 2.7.1.37), cAMP-dependent, catalytic chain - rat (fragment) [R.norvegicus]
268	17217	AA866299	a,j,k,w,x,y,z,jj, kk		ESTs
268	17218	AA866299	gg,jj,kk		ESTs
269	17742	AA866302	c	4-hydroxyphenylpyruvic acid dioxygenase	4-hydroxyphenylpyruvic acid dioxygenase
270	15935	AA866345	kk		ESTs
271	16607	AA866364	r		ESTs
272	11865	AA866383	d,ee,ff,kk		ESTs
273	15980	AA866426	s,ii		ESTs
274	15990	AA866439	b		ESTs
275	16001	AA866452	bb,cc,dd	Actin, alpha, cardiac	Actin, alpha, cardiac

TABLE 1					Atty. Ref: 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
276	309	AA866460	b		ESTs, Weakly similar to T42737 gp330 protein precursor - rat [R.norvegicus]
277	9391	AA866477	r		ESTs, Moderately similar to COXM_MOUSE Cytochrome c oxidase polypeptide VIIb, mitochondrial precursor [M.musculus]
278	16029	AA874803	j,k		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
278	16030	AA874803	j,k		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
279	16070	AA874873	cc,dd		ESTs
280	16074	AA874874	p,q	HMm:alcohol dehydrogenase 5	ESTs, Highly similar to ADHX_RAT ALCOHOL DEHYDROGENASE CLASS III (ALCOHOL DEHYDROGENASE 2) (GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE) (FDH) (FALDH) (ALCOHOL DEHYDROGENASE-B2) [R.norvegicus]
281	18563	AA874875	ii		
282	16082	AA874887	ii		ESTs, Weakly similar to segregation of mitotic chromosomes b; SMC (segregation of mitotic chromosomes 1)-like 1 (yeast) [Rattus norvegicus] [R.norvegicus]
283	16084	AA874889	r		ESTs
284	22781	AA874926	hh		ESTs, Weakly similar to dual-specificity phosphatase [Mus musculus] [M.musculus]
285	16139	AA874927	cc,dd		ESTs
286	15116	AA874928	f		ESTs, Highly similar to SNX4_HUMAN Sorting nexin 4 [H.sapiens]
287	16177	AA874952	ll		ESTs
288	17303	AA874990	u,v,w,x		ESTs, Weakly similar to RIKEN cDNA 6330407G11 [Mus musculus] [M.musculus]
289	16192	AA874995	jj,kk		ESTs
290	16215	AA874999	h,i,l,n,o		ESTs, Highly similar to protein translocation complex beta; protein transport protein SEC61 beta subunit [Homo sapiens] [H.sapiens]
291	16241	AA875019	l,m		ESTs, Highly similar to ZAP3_MOUSE Nuclear protein ZAP3 [M.musculus]
292	15573	AA875023	b,i,l,m		ESTs
293	16312	AA875032	j,k,p,q,bb,kk		ESTs
294	16319	AA875047	e		ESTs, Highly similar to TCPZ_MOUSE T-complex protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta) (CCT-zeta-1) [M.musculus]
295	16342	AA875060	s,t,jj,kk		ESTs
296	1190	AA875089	hh	Calpastatin	Calpastatin
297	16416	AA875098	n,o		ESTs, Highly similar to RIKEN cDNA 1110002O23 [Mus musculus] [M.musculus]
298	16419	AA875102	d		ESTs, Highly similar to RUXE_HUMAN Small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E) (Sm-E) (SmE) [M.musculus]
299	4339	AA875121	jj,kk	CCAAT binding factor of CBF-C/NFY-C	CCAAT binding factor of CBF-C/NFY-C
300	15310	AA875123	u,v		EST
301	15311	AA875124	ii		EST
302	11857	AA875132	d,ii		ESTs
303	14285	AA875194	ii		ESTs
304	15372	AA875205	y,z		ESTs, Highly similar to IF39_HUMAN Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) [H.sapiens]
305	18897	AA875207	t	Hemoglobin, beta	Hemoglobin, beta



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
306	15384	AA875217	cc,dd		ESTs
307	15887	AA875225	e	GTP-binding protein (G-alpha-i2)	GTP-binding protein (G-alpha-i2)
307	15888	AA875225	e,gg	GTP-binding protein (G-alpha-i2)	GTP-binding protein (G-alpha-i2)
308	15402	AA875261	d,jj,kk		ESTs
					ESTs, Highly similar to NUKM_HUMAN NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial precursor (Complex I-20KD) (CI-20KD) (PSST subunit) [H.sapiens]
309	15410	AA875268	jj,kk		ESTs
310	15440	AA875316	h,l		ESTs
311	15446	AA875327	n,o,s,t		ESTs
312	15510	AA875428	a,s,t,x,ee,ff,ll		ESTs
313	15513	AA875431	n,o		ESTs, Weakly similar to synbindin; syndecan binding protein 2 [Mus musculus] [M.musculus]
					ESTs, Highly similar to COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana); DNA segment, Chr 6, ERATO Doi 35, expressed; COP9 complex S7a; COP9 (constitutive photomorphogenic), subunit 7a (Arabidopsis) [Mus musculus] [M.musculus]
314	18864	AA875470	b		ESTs
315	15412	AA875500	r		ESTs
316	24470	AA875523	aa,bb		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
316	24471	AA875523	ii		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
316	24472	AA875523	ii		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
2	6153	AA875531	g,j,k	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	Rattus norvegicus CDK110 mRNA, procollagen, type I, alpha 2
317	15558	AA875537	y,z		ESTs, Highly similar to SFR2_MOUSE Splicing factor, arginine/serine-rich 2 (Splicing factor SC35) (SC-35) (Splicing component, 35 kDa) (PR264 protein) [M.musculus]
318	13051	AA875559	hh		ESTs
319	15617	AA875620	ee,ff,jj,kk		ESTs
319	15618	AA875620	y,z,ee,ff		ESTs
320	15629	AA875629	n,o,ll		ESTs
321	15638	AA875633	r,gg		ESTs
322	2846	AA875639	a		ESTs, Weakly similar to FAS_RAT FATTY ACID SYNTHASE [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14] [R.norvegicus]
323	15688	AA875664	aa		ESTs, Highly similar to mitochondria associated granulocyte macrophage CSF signaling molecule [Mus musculus] [M.musculus]
324	19388	AA891032	r		EST, Moderately similar to S37488 gene T10 protein - mouse [M.musculus]
325	5384	AA891041	j,k,p,q,y,z,kk	jun B proto-oncogene	jun B proto-oncogene
326	17057	AA891049	c		ESTs, Highly similar to PFD2_MOUSE Prefoldin subunit 2 [M.musculus]
327	19646	AA891054	c,p		ESTs
328	11940	AA891108	p,q,y,ee,ff		ESTs
329	18582	AA891207	u,ee,ff		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
330	24814	AA891209	n,o,w,x		ESTs, Highly similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligand [Mus musculus] [M.musculus]
331	21917	AA891220	h,l		ESTs
332	21928	AA891302	b,l,m		ESTs, Weakly similar to A53714 protein kinase (EC 2.7.1.37) BL44 - human [H.sapiens]
333	16446	AA891423	ii		ESTs
334	21938	AA891439	c		ESTs
335	13789	AA891476	jj,kk		ESTs
336	21951	AA891535	cc,dd		ESTs, Highly similar to hippocampus abundant gene transcript 1 [Mus musculus] [M.musculus]
337	19238	AA891542	d		ESTs
338	21905	AA891546	s		ESTs
339	15414	AA891551	p		ESTs
340	11949	AA891580	e		ESTs
341	11950	AA891595	e		ESTs
342	4447	AA891596	e,aa,bb		ESTs
343	4448	AA891631	ee,ff,jj,kk		ESTs
344	19321	AA891666	cc,dd	melanoma antigen, family D, 1	melanoma antigen, family D, 1
345	11387	AA891677	h,l,ll		ESTs
346	4459	AA891721	w,x		ESTs
347	17039	AA891727	aa		ESTs
348	23058	AA891733	a,l,m,ee,ff,jj,kk		ESTs
349	17255	AA891734	e,hh		ESTs
350	11959	AA891735	s		ESTs
351	17693	AA891737	u,v		ESTs
352	6535	AA891746	l,m		ESTs, Highly similar to endothelial differentiation-related factor 1; hypothetical protein 1-9 [Mus musculus] [M.musculus]
353	18269	AA891769	e		ESTs, Weakly similar to SC65 synaptonemal complex protein [Rattus norvegicus] [R.norvegicus]
354	9905	AA891774	l,m		ESTs
355	21672	AA891789	f,g		ESTs, Highly similar to MRGX_HUMAN Transcription factor-like protein MRGX (MORF-related gene X protein) [H.sapiens]
356	11966	AA891800	hh,jj,kk		ESTs, Weakly similar to F22G12.5.p [Caenorhabditis elegans] [C.elegans], ESTs, Weakly similar to IPYR_HUMAN Inorganic pyrophosphatase (Pyrophosphate phosphohydrolase) (PPase) [H.sapiens]
356	18128	AA891800	n,o		ESTs, Weakly similar to IPYR_HUMAN Inorganic pyrophosphatase (Pyrophosphate phosphohydrolase) (PPase) [H.sapiens]
357	23083	AA891802	cc,dd		ESTs
358	23011	AA891803	hh		ESTs
359	7050	AA891824	n,o		Rattus norvegicus clone ZG52 mRNA sequence
360	16023	AA891872	w,x		ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) [M.musculus]
361	19319	AA891937	f		ESTs, Highly similar to S66254 dolichyl-diphosphooligosaccharide-protein glycotransferase (EC 2.4.1.119) 50K chain - human [H.sapiens]
362	1159	AA891949	kk		ESTs
363	9826	AA891950	jj,kk		ESTs
364	4472	AA891962	ll		ESTs

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
365	4473	AA891965	jj,kk		ESTs, Highly similar to fructosamine 3 kinase [Mus musculus] [M.musculus]
366	4474	AA891969	b,l,m		ESTs
367	17374	AA891978	w,x,jj,kk		ESTs
368	15087	AA892010	s,t		ESTs, Weakly similar to T22242 hypothetical protein F45G2.10 - Caenorhabditis elegans [C.elegans]
369	17345	AA892014	hh	HLA-B associated transcript 1A	HLA-B associated transcript 1A
370	13420	AA892042	d,t,y,z		ESTs
371	8139	AA892094	ii		ESTs
372	23892	AA892120	s,t		ESTs
373	16899	AA892127	u,v		ESTs
374	12010	AA892137	jj,kk		ESTs, Highly similar to open reading frame 12 [Mus musculus] [M.musculus]
375	11384	AA892149	c,w		ESTs
376	20917	AA892238	f,ll		ESTs
377	17350	AA892240	l,m,ii		ESTs, Weakly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus]
378	22903	AA892250	d		ESTs, Highly similar to SYK_HUMAN Lysyl-tRNA synthetase (Lysine-tRNA ligase) (LysRS) [H.sapiens]
379	9073	AA892273	b		ESTs
380	18190	AA892280	a,s,t,w,x		ESTs
381	11982	AA892284	ii		ESTs
382	18209	AA892318	s,t		ESTs, Highly similar to JC7219 nuclear protein SR-25 - mouse [M.musculus]
383	13647	AA892367	w,x,cc,dd		ESTs, Highly similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus]
384	15492	AA892376	f		ESTs
385	3473	AA892378	e		ESTs, Weakly similar to F13B9.8.p [Caenorhabditis elegans] [C.elegans]
385	3474	AA892378	e,gg		ESTs, Weakly similar to F13B9.8.p [Caenorhabditis elegans] [C.elegans]
386	2832	AA892388	b,u,v	CD59 antigen	CD59 antigen
387	22868	AA892391	ee,ff		ESTs, Weakly similar to TC17_RAT Zinc finger protein 354A (Transcription factor 17) (Renal transcription factor Kid-1) (Kidney, ischemia, and developmentally regulated protein-1) [R.norvegicus]
388	14754	AA892414	gg		ESTs
389	23194	AA892417	gg	ephrin A1	ephrin A1
390	9254	AA892470	e		ESTs, Highly similar to S03644 histone H2A.Z - rat [R.norvegicus]
391	11992	AA892485	f	dihydrolipoamide acetyltransferase	dihydrolipoamide acetyltransferase
392	1522	AA892486	c		ESTs, Weakly similar to A36690 sucrose alpha-glucosidase (EC 3.2.1.48) - rat (fragment) [R.norvegicus]
393	24873	AA892498	jj,kk		ESTs, Weakly similar to CD63_RAT CD63 antigen (AD1 antigen) [R.norvegicus]
394	14066	AA892504	s,t,u		ESTs
395	11994	AA892507	hh		ESTs, Moderately similar to S63540 protein DS 1, 24K - human [H.sapiens]
396	23888	AA892520	w,x		ESTs
396	23889	AA892520	w,x		ESTs
397	8599	AA892522	r		ESTs
398	17468	AA892545	t		ESTs, Moderately similar to organic cationic transporter-like 2 [Mus musculus] [M.musculus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
399	16507	AA892547	cc,dd		ESTs, Highly similar to hypothetical protein CL25022 [Homo sapiens] [H.sapiens]
400	11202	AA892554	r		ESTs
400	11203	AA892554	j,k		ESTs
401	13574	AA892557	jj,kk		ESTs
402	18274	AA892572	gg,hh		ESTs, Highly similar to RIKEN cDNA 1110001J03 [Mus musculus] [M.musculus]
402	18275	AA892572	hh		ESTs, Highly similar to RIKEN cDNA 1110001J03 [Mus musculus] [M.musculus]
403	4512	AA892578	j,k,p,q		ESTs
404	15876	AA892582	g,w,x		ESTs, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [R.norvegicus]
405	19085	AA892598	j,k,y,z,ee,ff,kk		ESTs, Weakly similar to putative nucleotide binding protein, estradiol-induced [Homo sapiens] [H.sapiens]
405	19086	AA892598	j,k,p,q,y,z		ESTs, Weakly similar to putative nucleotide binding protein, estradiol-induced [Homo sapiens] [H.sapiens]
406	2119	AA892607	gg		ESTs
407	4517	AA892642	f		ESTs
408	20065	AA892647	c,d,r	germinal histone H4 gene	germinal histone H4 gene
409	23783	AA892773	w,x		ESTs
410	12118	AA892775	a,n,x	Lysozyme	Lysozyme
411	21972	AA892791	ii		ESTs, Highly similar to ERC1_MOUSE DNA EXCISION REPAIR PROTEIN ERCC-1 [M.musculus]
412	11997	AA892828	f,h,l	HMm:pyruvate dehydrogenase (lipoamide) beta	ESTs, Highly similar to S15892 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - rat [R.norvegicus]
413	7148	AA892842	f,g		ESTs, Weakly similar to CAZ3_RAT F-actin capping protein alpha-3 subunit (CAPZ alpha-3) [R.norvegicus]
414	17923	AA892843	b		ESTs, Moderately similar to hypothetical protein FLJ20917 [Homo sapiens] [H.sapiens]
415	17589	AA892851	p,q,s,t		ESTs
415	17590	AA892851	a,j,k		ESTs
416	22871	AA892859	gg		ESTs, Weakly similar to PLO1_RAT Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor (Lysyl hydroxylase 1) (LH1) [R.norvegicus]
417	18888	AA892860	a		ESTs
418	1031	AA892863	t		ESTs
419	12848	AA892916	s,t		ESTs, Weakly similar to JC7260 strictosidine synthase (EC 4.3.3.2) homolog 2 - fruit fly (Drosophila melanogaster) [D.melanogaster]
420	24279	AA892919	d	nucleolar phosphoprotein p130	nucleolar phosphoprotein p130
421	16482	AA892940	gg		ESTs, Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus]
422	15956	AA892942	d		ESTs
423	19124	AA893022	ii		ESTs, Weakly similar to GSHH_RAT Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (PHGPx) (GPX-4) [R.norvegicus]
424	14360	AA893043	h,l		ESTs
425	12022	AA893105	u,v,ii		ESTs
426	22423	AA893164	m		ESTs
427	17731	AA893194	c,f		ESTs, Moderately similar to hypothetical protein MGC10974 [Homo sapiens] [H.sapiens]
428	13323	AA893212	hh		ESTs
429	4243	AA893217	f		ESTs

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
430	3879	AA893237	e		ESTs, Moderately similar to hypothetical protein MBC3205 [Homo sapiens] [H.sapiens]
431	20985	AA893242	ll	fatty acid Coenzyme A ligase, long chain 2	fatty acid Coenzyme A ligase, long chain 2
431	20986	AA893242	ll	fatty acid Coenzyme A ligase, long chain 2	fatty acid Coenzyme A ligase, long chain 2
432	17752	AA893244	ii		ESTs
433	21652	AA893267	u,v		ESTs, Weakly similar to S46992 protein p130 - rat [R.norvegicus]
434	16168	AA893280	a,y,z		ESTs, Moderately similar to ADFP_MOUSE ADIPOPHILIN (ADIPOSE DIFFERENTIATION-RELATED PROTEIN) (ADRP) [M.musculus]
435	11935	AA893328	gg		ESTs, Moderately similar to C54354 calnexin precursor - rat [R.norvegicus]
436	22355	AA893338	b,u,v		Rattus norvegicus hypothetical RNA binding protein RDA288 mRNA, complete cds
437	9082	AA893357	gg		ESTs
438	18542	AA893493	g		ESTs, Highly similar to RL26_RAT 60S RIBOSOMAL PROTEIN L26 [R.norvegicus]
439	2689	AA893515	ll		ESTs, Highly similar to translocation protein 1; Dtrp1 protein; membrane protein SEC62, S.cerevisiae, homolog of [Homo sapiens] [H.sapiens]
440	22891	AA893581	f		ESTs
441	22149	AA893607	s,t		ESTs
441	22150	AA893607	b,l,m		ESTs
442	4541	AA893612	e		ESTs
443	19505	AA893634	r,ii		ESTs, Moderately similar to coatomer protein complex, subunit zeta 1; nonclathrin coat protein zeta1-COP [Mus musculus] [M.musculus]
444	3623	AA893663	jj,kk		ESTs
445	4544	AA893664	h,l	TEMO	TEMO
446	19411	AA893667	cc,dd		ESTs, Weakly similar to T46904 hypothetical protein DKFZp761D081.1 - human [H.sapiens]
447	9084	AA893717	d		ESTs
448	22731	AA893743	f,g		ESTs
449	4556	AA893811	aa,bb		ESTs
450	12031	AA893860	y,z	HHs:threonyl-tRNA synthetase	ESTs, Moderately similar to SYTC_HUMAN Threonyl-tRNA synthetase, cytoplasmic (Threonine-tRNA ligase) (ThrRS) [H.sapiens]
451	17896	AA893905	ii		ESTs
452	3446	AA893970	h,aa,bb		ESTs
453	22145	AA893980	ii		ESTs
454	4565	AA893994	b,l,m		EST
455	23731	AA894004	l,n,o,kk,ll		ESTs, Highly similar to CAPG_MOUSE Macrophage capping protein (Myc basic motif homolog-1) (Actin-capping protein GCAP39) [M.musculus]
456	22583	AA894009	b,l,m		
456	22584	AA894009	aa,bb,ii		ESTs
457	10540	AA894027	r		
458	15913	AA894092	n,o		ESTs
459	16485	AA894104	jj,kk		ESTs, Weakly similar to T20253 hypothetical protein F53E4.1 - Caenorhabditis elegans [C.elegans]
460	9388	AA894173	c		ESTs
461	16434	AA894174	h,l		ESTs, Highly similar to A31568 electron transfer flavoprotein alpha chain precursor - rat [R.norvegicus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
462	21989	AA894188	cc,dd		ESTs
463	2133	AA894193	r		ESTs
464	24473	AA894200	b		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
465	22783	AA894207	r		ESTs, Weakly similar to dual-specificity phosphatase [Mus musculus] [M.musculus]
466	3929	AA894233	s		ESTs
467	17336	AA894297	j,k,s,t		ESTs
468	3910	AA894345	f,j,k,r,gg		ESTs, Weakly similar to 2021425A MAT1 gene [Mus musculus] [M.musculus]
469	4107	AA899109	d		ESTs
470	24329	AA899253	aa,bb	Myristoylated alanine-rich protein kinase C substrate	Myristoylated alanine-rich protein kinase C substrate
471	22490	AA899289	d		ESTs, Moderately similar to KIAA1049 protein [Homo sapiens] [H.sapiens]
472	4636	AA899491	e		ESTs, Highly similar to SYW_MOUSE Tryptophanyl-tRNA synthetase (Tryptophan-tRNA ligase) (TrpRS) [M.musculus]
473	22308	AA899535	u,v		ESTs
474	20038	AA899797	bb,ll		EST
475	2559	AA899828	l,m		ESTs
476	23778	AA899854	c	topoisomerase (DNA) II alpha	topoisomerase (DNA) II alpha
477	17243	AA899894	r		ESTs, Highly similar to S30034 translocating chain-associating membrane protein - human [H.sapiens]
478	21639	AA899911	ll		ESTs
479	9114	AA899951	cc,dd		ESTs
480	17355	AA899959	l,m		ESTs, Highly similar to S63993 acrosomal protein AZ1 - mouse [M.musculus]
481	18890	AA899964	e,r		ESTs
482	11268	AA899969	l,m		ESTs, Highly similar to T08712 hypothetical protein DKFZp566C0424.1 - human (fragment) [H.sapiens]
483	3903	AA899986	w,x	polypyrimidine tract binding protein	polypyrimidine tract binding protein
484	22480	AA900230	u,v		ESTs, Weakly similar to T12B3.4.p [Caenorhabditis elegans] [C.elegans]
485	4725	AA900290	t,y,z,ee,ff	HMm:carbon catabolite repression 4 homolog (S. cerevisiae)	ESTs, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus]
486	4730	AA900326	d,jj,kk		ESTs
487	4732	AA900343	cc,dd		ESTs, Weakly similar to T47146 hypothetical protein DKFZp761C169.1 - human (fragment) [H.sapiens]
488	4750	AA900469	u,v		ESTs
489	16753	AA900474	w,x		ESTs, Moderately similar to T50619 hypothetical protein DKFZp762M136.1 - human (fragment) [H.sapiens]
490	4774	AA900762	ii		ESTs
491	4779	AA900825	u,v		ESTs
492	14712	AA900860	ee,ff		ESTs, Weakly similar to COPP_RAT Coatamer beta' subunit (Beta'-coat protein) (Beta'-COP) (p102) [R.norvegicus]
493	3822	AA900863	kk		ESTs, Weakly similar to HE47_RAT Probable ATP-dependent RNA helicase p47 [R.norvegicus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
494	4790	AA900875	ee,ff	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
495	23038	AA900881	a,j,k,y,z	branched chain aminotransferase 1, cytosolic	branched chain aminotransferase 1, cytosolic
496	4797	AA900967	j,k		ESTs
497	22666	AA900974	a,t,y,z,ee,ff		ESTs, Highly similar to p34SEI-1; PHD zinc finger- and bromodomain-interacting protein 1 [Mus musculus] [M.musculus]
498	26075	AA900993	s,t		
499	4827	AA901058	gg		ESTs
500	11467	AA901069	j,k		
501	22898	AA901107	kk		ESTs
502	4858	AA901238	w,x		ESTs, Weakly similar to S53358 ubiquitin-conjugating enzyme E2.17kB - rat [R.norvegicus]
503	4861	AA901290	y,z,kk		ESTs
504	16976	AA901341	j,k		ESTs, Highly similar to sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase B; ST6GalNAc II [Mus musculus] [M.musculus]
505	4866	AA901350	d		ESTs
506	4874	AA923850	kk		ESTs
507	4893	AA923996	h,l		EST
508	18162	AA924013	r		ESTs
509	17644	AA924036	c,kk		ESTs
510	4907	AA924091	r		ESTs, Weakly similar to growth suppressor 1; leprecan [Rattus norvegicus] [R.norvegicus]
511	4909	AA924097	jj,kk		ESTs
512	17231	AA924107	ii	Tissue inhibitor of metalloproteinase 3	Tissue inhibitor of metalloproteinase 3
513	4917	AA924140	l,m		ESTs, Weakly similar to Y193_HUMAN
514	4930	AA924251	c		Hypothetical protein KIAA0193 [H.sapiens]
515	22914	AA924335	h,l,ll		ESTs
516	12346	AA924346	d,aa,bb		ESTs
517	23096	AA924352	b,v		ESTs, Weakly similar to Prostatic Acid Phosphatase (E.C.3.1.3.2) Complexed With Tartaric Acid [R.norvegicus]
518	4945	AA924415	n,o		ESTs
519	4954	AA924444	u,v		ESTs
520	18251	AA924548	jj,kk		ESTs, Highly similar to RL9_RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus]
521	4975	AA924571	l,m		ESTs
522	24310	AA924578	g,ll		ESTs
523	18891	AA924598	e		ESTs
524	5002	AA924689	ii		ESTs
525	23123	AA924794	a,kk		ESTs
526	5030	AA924802	e		ESTs
527	2888	AA924902	w,x		ESTs
528	20953	AA924926	h,l,jj,kk		ESTs
529	22911	AA924943	l,m		ESTs
530	168	AA924985	e	calsequestrin 2	calsequestrin 2
531	5070	AA925031	r		ESTs
532	23173	AA925057	h,l,w,x		ESTs, Highly similar to GYRTI cysteine-rich intestinal protein - rat [R.norvegicus]
533	17363	AA925150	ll		ESTs, Moderately similar to 2118320A neurodegeneration-associated protein 1 [Rattus norvegicus] [R.norvegicus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
534	18271	AA925267	e		ESTs
535	23452	AA925289	gg		ESTs, Moderately similar to hypothetical protein MGC8974 [Homo sapiens] [H.sapiens]
536	16499	AA925300	p,ee,ff,gg	HHs:mitogen-activated protein kinase kinase kinase 3	ESTs, Weakly similar to mitogen activated protein kinase kinase kinase 1 [Rattus norvegicus] [R.norvegicus]
537	5129	AA925335	t		ESTs
538	5132	AA925342	h,l		ESTs, Highly similar to MYM1_MOUSE Myomesin 1 (Skelemin) [M.musculus]
539	23978	AA925352	kk,ll		ESTs
540	21500	AA925353	w,x,cc,dd		ESTs
541	14945	AA925364	n,o		ESTs
542	5167	AA925529	ee,ff		EST
543	4285	AA925708	r,y,z,jj,kk		ESTs, Moderately similar to WDR1_MOUSE WD-repeat protein 1 (Actin interacting protein 1) [M.musculus]
544	5206	AA925755	ll	Glutaminase	Glutaminase
545	3997	AA925771	ii		ESTs, Highly similar to T12483 hypothetical protein DKFZp564B0769.1 - human (fragment) [H.sapiens]
546	23464	AA925876	l,m		ESTs
547	5227	AA925924	l,o,kk		ESTs, Highly similar to cytokine receptor-like factor 1; cytokine receptor like molecule 3 [Mus musculus] [M.musculus]
548	20345	AA925938	gg		ESTs
549	5258	AA926089	t		ESTs, Highly similar to KIAA0164 gene product [Homo sapiens] [H.sapiens]
550	17157	AA926129	cc		ESTs
551	16468	AA926137	hh		ESTs, Moderately similar to UCRY_HUMAN Ubiquinol-cytochrome C reductase complex 6.4 kDa protein (Complex III subunit XI) [H.sapiens]
552	20327	AA926265	cc,dd		EST, Weakly similar to ADP-ribosylation factor-like 5 [Rattus norvegicus] [R.norvegicus]
553	893	AA926305	h,l		ESTs
553	894	AA926305	h,l,n,o		ESTs
554	3817	AA926328	p,q	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
555	9942	AA942697	d		ESTs, Highly similar to hypothetical protein MGC3133 [Homo sapiens] [H.sapiens]
556	16909	AA942704	g		ESTs, Moderately similar to SUR2_MOUSE Surfeit locus protein 2 (Surf-2) [M.musculus]
557	6039	AA942716	d		ESTs, Highly similar to hematological and neurological expressed sequence 1 [Mus musculus] [M.musculus]
558	22677	AA942718	s,t,kk	B cell lymphoma 2 like	B cell lymphoma 2 like
559	23005	AA942770	e,y,z		ESTs
560	17003	AA942930	ll		ESTs
561	19016	AA943015	cc,dd		ESTs
562	3952	AA943016	u,v		ESTs
563	22130	AA943020	jj,kk		ESTs
564	6691	AA943028	r,w,x		ESTs, Highly similar to KFMS_RAT Macrophage colony stimulating factor I receptor precursor (CSF-1-R) (Fms proto-oncogene) (c-fms) [R.norvegicus]
565	2675	AA943099	cc,dd		ESTs
566	23822	AA943114	ll		ESTs
567	22187	AA943229	u,v		EST



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
568	12261	AA943240	gg		ESTs, Weakly similar to one twenty two protein; hypothetical protein FLJ12479 [Homo sapiens] [H.sapiens]
569	22218	AA943409	e		ESTs
570	22223	AA943440	w,x		EST
571	21990	AA943524	b		ESTs
572	22247	AA943537	y,z	zyxin	zyxin
572	22248	AA943537	y,z	zyxin	zyxin
573	22261	AA943573	d		ESTs
574	19220	AA943740	jj,kk		ESTs
575	9658	AA943748	t		ESTs
576	22317	AA943766	j,k		ESTs, Moderately similar to ASPG_MOUSE N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase precursor (Glycosylasparaginase) (Aspartylglucosaminidase) (N4-(N-acetyl-beta-glucosaminyl)-L-asparagine amidase) (AGA) [M.musculus]
577	11412	AA943981	ii		ESTs
577	11413	AA943981	r		ESTs
578	16447	AA944188	gg		ESTs
579	22378	AA944212	a,y,z,ee,ff,kk		ESTs
580	22381	AA944216	j,k		ESTs
581	22405	AA944341	u,v		ESTs
582	15596	AA944353	jj,kk		ESTs
583	12289	AA944383	gg		ESTs
584	20795	AA944397	e,ee	HMm:heat shock protein, 86 kDa 1	ESTs, Moderately similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
585	21998	AA944398	gg		ESTs, Highly similar to A49457 fibulin-2 precursor - mouse [M.musculus]
586	22681	AA944413	p,q		ESTs
587	15476	AA944426	h,l	Calmodulin III	Calmodulin III
588	19480	AA944442	r,bb		ESTs, Weakly similar to SLI3_RAT SKELETAL MUSCLE LIM-PROTEIN 3 (SLIM 3) (LIM-DOMAIN PROTEIN DRAL) (FOUR AND A HALF LIM DOMAINS PROTEIN 2) (FHL-2) [R.norvegicus]
589	21522	AA944449	gg		ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]
590	22431	AA944463	r		ESTs
591	14763	AA944481	p,q		ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]
592	2661	AA944493	d		ESTs
593	22438	AA944498	l,m		ESTs
594	22678	AA944556	jj,kk		ESTs
595	12303	AA944786	t		ESTs
596	22536	AA944803	r		ESTs
597	22081	AA944818	j,k,jj,kk		ESTs
598	21581	AA944828	bb		ESTs, Highly similar to RIKEN cDNA 2610524G07 [Mus musculus] [M.musculus]
599	21973	AA944840	s,t		ESTs, Weakly similar to T19073 hypothetical protein C08B11.9 - Caenorhabditis elegans [C.elegans]
600	22667	AA945069	p,q,y,z		ESTs, Highly similar to p34SEI-1; PHD zinc finger- and bromodomain-interacting protein 1 [Mus musculus] [M.musculus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
601	22556	AA945100	w,x		ESTs
3	19421	AA945152	bb	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	dimethylarginine dimethylaminohydrolase 1
602	22283	AA945172	e	HHs:leucine aminopeptidase 3	ESTs, Highly similar to AMPL_HUMAN Cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Proline aminopeptidase) (Prolyl aminopeptidase) [H.sapiens]
603	14352	AA945181	gg		ESTs
604	4207	AA945591	n,o,w,x		ESTs, Weakly similar to JC5105 stromal cell-derived factor 2 - mouse [M.musculus]
605	22266	AA945601	hh		ESTs
605	22267	AA945601	gg		ESTs
606	24521	AA945636	g,h,l		ESTs, Highly similar to R5RT12 acidic ribosomal protein P1, cytosolic [validated] - rat [R.norvegicus]
607	22615	AA945643	kk		ESTs, Moderately similar to C3L1_MOUSE Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39) (GP-39) (BRP39 protein) [M.musculus]
608	11871	AA945679	j,k		ESTs
609	22625	AA945704	p,q,ee,ff,ii		ESTs
610	23035	AA945712	t		ESTs
611	20619	AA945737	d,r,aa,bb	Chemokine receptor (LCR1)	Chemokine receptor (LCR1)
612	14955	AA945750	t		ESTs
613	3637	AA945878	u,v		ESTs
614	11256	AA945898	gg		ESTs
615	22682	AA945910	cc,dd		ESTs
616	21351	AA945932	t	Annexin A3	Annexin A3
617	22692	AA945986	jj,kk		ESTs
618	22697	AA945996	j,k,kk		ESTs
619	20832	AA946040	hh		ESTs, Highly similar to COXG_MOUSE Cytochrome c oxidase polypeptide VIb (AED) [M.musculus]
620	18337	AA946046	l,m		ESTs
621	22708	AA946063	u,v		ESTs, Highly similar to ubiquitin-like 3 [Homo sapiens] [H.sapiens]
622	22711	AA946072	r,y,z,kk		ESTs, Highly similar to catenin alpha-like 1; alpha-catenin related protein [Mus musculus] [M.musculus]
623	12324	AA946203	n,o		ESTs
624	23237	AA946224	ii		ESTs
625	23027	AA946264	aa,bb		ESTs
626	19387	AA946275	a		ESTs, Highly similar to AR21_HUMAN ARP2/3 complex 21 kDa subunit (P21-ARC) (Actin-related protein 2/3 complex subunit 3) [H.sapiens]
627	22755	AA946323	ii		ESTs
628	884	AA946362	ii		ESTs, Highly similar to SNX5_MOUSE Sorting nexin 5 [M.musculus]
629	9629	AA946415	gg		ESTs
630	22771	AA946432	b,l,m	casein kinase I delta	casein kinase I delta
631	643	AA946439	d		ESTs, Highly similar to HSRT4 histone H4 - rat [R.norvegicus]
632	2363	AA946469	hh		ESTs
633	22042	AA946476	e		ESTs
634	23471	AA955162	j,k,s,t		ESTs
635	9452	AA955206	y,z,ee,ff		ESTs
636	22439	AA955213	ii		ESTs
637	23498	AA955248	w,x		ESTs

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638	22596	AA955298	y,z		ESTs, Weakly similar to T46637 transcription factor 1, neural - rat [R.norvegicus]
639	23326	AA955415	n,o		ESTs
640	23626	AA955540	p,q		ESTs
641	12928	AA955564	e		ESTs, Weakly similar to T21697 hypothetical protein F40E10.6 - Caenorhabditis elegans [C.elegans]
642	23673	AA955684	s,t		ESTs
643	5111	AA955729	f,g,l,m		EST, ESTs, Highly similar to OKRT2R protein kinase (EC 2.7.1.37), cAMP-dependent, type II-alpha regulatory chain - rat (fragment) [R.norvegicus]
644	12426	AA955760	u,v		ESTs, Weakly similar to LIS1_MOUSE Platelet-activating factor acetylhydrolase IB alpha subunit (PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH alpha) (PAFAH alpha) (Lissencephaly-1 protein) (LIS-1) [R.norvegicus]
645	6658	AA955857	b,c,l,m		ESTs, Highly similar to TRBP_MOUSE TAR RNA-binding protein 2 (Protamine-1 RNA binding protein) (PRM-1 RNA binding protein) [M.musculus]
646	17540	AA955914	a		EST, EST, Moderately similar to FBRL_MOUSE Fibrillarin (Nucleolar protein 1) [M.musculus], ESTs, Highly similar to S38342 fibrillarin - mouse [M.musculus]
647	14327	AA956111	h,l		ESTs, Moderately similar to T43493 hypothetical protein DKFZp434C119.1 - human [H.sapiens]
648	23357	AA956114	cc,dd		ESTs, Highly similar to ubiquitin conjugating enzyme [Rattus norvegicus] [R.norvegicus]
649	498	AA956278	aa,bb		ESTs
650	23409	AA956294	e		ESTs
651	5210	AA956550	j,k		ESTs
652	22899	AA956555	r,kk		ESTs
653	23840	AA956689	l,m		EST
654	18296	AA956703	w,x		ESTs
655	17495	AA956733	b		ESTs
656	16543	AA956758	l,m		EST
657	5990	AA956907	u,v		ESTs, Highly similar to IF3A_MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN) (CENTROSOMIN) [M.musculus]
658	23927	AA957007	g	glutathione S-transferase, mu 5	glutathione S-transferase, mu 5
659	23952	AA957096	gg		ESTs
660	23957	AA957123	c		ESTs, Weakly similar to NADE_HUMAN p75NTR-associated cell death executor (Nerve growth factor receptor associated protein 1) (Ovarian granulosa cell 13.0 kDa protein HGR74) [H.sapiens]
661	23963	AA957139	kk		ESTs
662	19283	AA957259	l,m		EST
663	23314	AA957270	p,q,ee,ff		ESTs
664	24012	AA957335	b,d		ESTs
665	12529	AA957362	d	transforming growth factor beta 1 induced transcript 1	transforming growth factor beta 1 induced transcript 1
666	24040	AA957422	n,o,w,x		ESTs, Highly similar to FCEG_RAT High affinity immunoglobulin epsilon receptor gamma-subunit precursor (FcERI) (IgE Fc receptor gamma-subunit) (Fc-epsilon RI-gamma) [R.norvegicus]

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
667	24051	AA957452	a,jj,kk		ESTs
668	3669	AA957535	a		ESTs
669	23732	AA957653	ee,ff		ESTs, Weakly similar to RNB6 [Rattus norvegicus] [R.norvegicus]
670	24135	AA957736	n,o		ESTs, Weakly similar to FBL5_RAT Fibulin-5 precursor (FBL-5) (Developmental arteries and neural crest EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing protein) (EVEC) [R.norvegicus]
671	23644	AA957808	gg		ESTs, Weakly similar to SNX9_HUMAN Sorting nexin 9 (SH3 and PX domain-containing protein 1) (SDP1 protein) [H.sapiens]
672	24171	AA957835	jj,kk,ll		ESTs
673	23831	AA963094	d		ESTs
674	11500	AA963171	cc,dd		ESTs, Weakly similar to heterogeneous nuclear ribonucleoprotein A/B [Rattus norvegicus] [R.norvegicus]
675	23289	AA963173	ii		ESTs
676	3953	AA963260	s,t		ESTs, Moderately similar to A46613 protein 4.1, P4.1 - mouse [M.musculus]
677	2173	AA963627	w,x		ESTs
678	24246	AA963703	a		ESTs, Highly similar to P2G4_MOUSE Proliferation-associated protein 2G4 (Proliferation-associated protein 1) (Protein p38-2G4) [M.musculus]
679	2195	AA963746	r		ESTs
680	6276	AA963767	b,c,u,v		ESTs
681	2211	AA963834	l,m		ESTs, Highly similar to S105_MOUSE S100 calcium-binding protein A5 (S-100D protein) [R.norvegicus]
682	2214	AA963838	b		ESTs
683	2301	AA964206	a		ESTs
684	2321	AA964265	ll		ESTs
685	2095	AA964362	cc,dd		ESTs
686	2373	AA964455	jj,kk		ESTs
687	18830	AA964496	a,z		ESTs, Highly similar to ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin) [R.norvegicus]
688	2378	AA964501	t		ESTs
689	2142	AA964526	c		ESTs, Weakly similar to C35D10.4.p [Caenorhabditis elegans] [C.elegans]
690	2410	AA964589	kk		EST, ESTs
691	14342	AA964595	h,l,s,t		ESTs, Moderately similar to treacle [Mus musculus] [M.musculus]
692	19145	AA964613	l,m		ESTs
693	2424	AA964617	u,v		ESTs
694	2459	AA964755	a,q,y,z,ee,ff		ESTs
695	2476	AA964841	cc,dd		EST
696	2492	AA964866	u,v		ESTs, Moderately similar to A49947 interferon gamma receptor beta subunit - mouse [M.musculus]
697	17232	AA965161	ll	Tissue inhibitor of metalloproteinase 3	Tissue inhibitor of metalloproteinase 3
698	2582	AA965164	gg		ESTs, Moderately similar to RIKEN cDNA 1810017F10 [Mus musculus] [M.musculus]
699	15885	AA965207	t		ESTs, Highly similar to T14795 hypothetical protein DKFZp434E171.1 - human (fragment) [H.sapiens]
700	2803	AA996451	r,jj,kk		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
701	2861	AA996583	ee,ff		ESTs, Weakly similar to T18768 hypothetical protein B0491.7 - <i>Caenorhabditis elegans</i> [C.elegans]
702	2880	AA996658	b		EST
703	19396	AA996740	n,o		EST, Moderately similar to A54981 TBD-associated factor 30 - human [H.sapiens]
704	17492	AA996832	l,m		ESTs, Moderately similar to hypothetical protein FLJ11219 [Homo sapiens] [H.sapiens]
705	2962	AA996953	u,v		ESTs
706	16496	AA996955	w,x		ESTs
707	8786	AA996993	d		EST, Moderately similar to RED_MOUSE Red protein (RER protein) [M.musculus], ESTs, Highly similar to RED_MOUSE Red protein (RER protein) [M.musculus]
708	3132	AA997191	h,l		EST
709	3162	AA997289	gg		ESTs
710	3003	AA997330	e,t,kk		ESTs
711	21942	AA997341	e		ESTs
712	3165	AA997386	n,o		ESTs, Weakly similar to S27393 sphingomyelin phosphodiesterase (EC 3.1.4.12), acidic, splice form 1 precursor - mouse [M.musculus]
713	14582	AA997412	r		ESTs
714	3207	AA997466	j,k,ee,ff,kk		ESTs
715	3242	AA997596	d		ESTs
716	21119	AA997655	b		ESTs, Highly similar to hypothetical protein FLJ14566 [Homo sapiens] [H.sapiens]
717	3043	AA997694	jj,kk		ESTs
718	3250	AA997765	h,l,il	fibrillin-1	fibrillin-1
719	3257	AA997766	ii		ESTs
720	3265	AA997784	u,v		EST
721	3269	AA997800	c		ESTs, Moderately similar to T30249 cell proliferation antigen Ki-67 - mouse [M.musculus]
722	2757	AA997851	bb,ll		ESTs, Weakly similar to A41220 transforming growth factor beta receptor type III precursor - rat [R.norvegicus]
723	3290	AA997883	ee,ff		ESTs
724	26114	AA997904	aa,bb		
725	10614	AA997985	cc,dd		ESTs
726	3332	AA998006	ll		ESTs
727	3353	AA998053	ii		ESTs, ESTs, Weakly similar to MOZ_HUMAN Monocytic leukemia zinc finger protein (Zinc finger protein 220) [H.sapiens]
728	3511	AA998152	ee,ff	brain-specific angiogenesis inhibitor 1-associated protein 2	brain-specific angiogenesis inhibitor 1-associated protein 2
729	16533	AA998174	kk		ESTs
730	3390	AA998195	u,v		ESTs, Weakly similar to S37694 gene PC326 protein - mouse [M.musculus]
731	6789	AA998207	b,d		ESTs
732	3738	AA998256	y,z		ESTs
733	19458	AA998345	w,x		EST
734	3781	AA998375	b,u,v		ESTs
735	3505	AA998430	w,x	adrenergic receptor kinase, beta 1	adrenergic receptor kinase, beta 1
736	2782	AA998565	c,l,m		ESTs, Moderately similar to CDNC_MOUSE CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2) [M.musculus]
737	22737	AA998660	ii		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
738	2526	AA998979	u,v		ESTs, Moderately similar to T00051 hypothetical protein KIAA0404 - human (fragment) [H.sapiens]
739	12664	AA999110	a,ee,ff,kk		ESTs, Weakly similar to MAPE_HUMAN Melanoma antigen preferentially expressed in tumors (Preferentially expressed antigen of melanoma) (OPA-interacting protein 4) (OIP4) [H.sapiens]
740	25137	AB005540	cc,dd		
741	11745	AB006450	hh,jj,kk	translocator of inner mitochondrial membrane 17 kDa, a	translocator of inner mitochondrial membrane 17 kDa, a
742	21666	AB012214	n,o	DNA (cytosine-5-)-methyltransferase 1	ESTs, Highly similar to JE0378 DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - rat [R.norvegicus]
743	17963	AB012231	jj,kk	nuclear factor I/B	nuclear factor I/B
744	15772	AB015645	cc,dd		Rattus norvegicus mRNA for G protein-coupled receptor, complete cds
745	22567	AB017544	aa	peroxisomal membrane anchor protein	peroxisomal membrane anchor protein
746	3799	AF002281	p,u,v,ee,ff,kk,ll	actinin alpha 2 associated LIM protein	actinin alpha 2 associated LIM protein
747	1097	AF016296	e,j,k,cc,dd,kk		Rattus norvegicus neuropilin mRNA, complete cds
748	19649	AF016387	jj,kk	retinoid X receptor gamma (	retinoid X receptor gamma (
748	19650	AF016387	jj,kk	retinoid X receptor gamma (	retinoid X receptor gamma (
749	23044	AF034218	j,k	hyaluronidase 2	hyaluronidase 2
750	19058	AF054618	ee,ff	cortactin isoform B	cortactin isoform B
751	2881	AF056034	b,d,u,v	nexilin	nexilin
752	16006	AF062594	gg	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
752	16007	AF062594	hh	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
753	20741	AF084186	s,t	alpha-fodrin	alpha-fodrin
754	21957	AF087437	f	core binding factor beta	ESTs
755	18731	AF093139	d	tip associating protein	tip associating protein
756	2947	AF099093	u,v	ubiquitin-conjugating enzyme UBC7	ubiquitin-conjugating enzyme UBC7
757	25232	AF110508	b		
758	21757	AI007656	d		ESTs
759	9976	AI007744	e,jj,kk		ESTs
760	4018	AI007770	j,k		ESTs
4	1804	AI007824	j	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	
761	10108	AI007857	u,v	HGF-regulated tyrosine kinase substrate	HGF-regulated tyrosine kinase substrate
762	11728	AI007884	t		ESTs
763	11368	AI007948	l,m		ESTs, Highly similar to RIKEN cDNA 1500006O09 [Mus musculus] [M.musculus]
764	15849	AI008074	r,ll		ESTs, ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
765	4052	AI008095	jj,kk		ESTs
766	2657	AI008275	u,v		ESTs, Weakly similar to YJ95_CAEEL HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [C.elegans]
767	21229	AI008371	r		ESTs
768	21889	AI008393	u,v		ESTs, Highly similar to UBX domain-containing 2 [Mus musculus] [M.musculus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
769	3808	AI008643	p,q,ee,ff		ESTs, Weakly similar to DJB1_MOUSE DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) (Heat shock protein 40) (HSP40) [M.musculus]
770	11325	AI008647	y,z		ESTs
771	12398	AI008689	s,t		ESTs, Weakly similar to TAC1_HUMAN Transforming acidic coiled-coil-containing protein 1 [H.sapiens]
772	3931	AI008697	n,o		ESTs, Highly similar to ACES_RAT Acetylcholinesterase precursor (AChE) [R.norvegicus]
773	16034	AI008701	u,v		ESTs
774	7785	AI008758	jj,kk	Dipeptidyl peptidase 4	Dipeptidyl peptidase 4
775	18125	AI008787	f,g		ESTs, Highly similar to S16788 probable reverse transcriptase - rat [R.norvegicus]
776	12828	AI008796	cc,dd		ESTs
777	3832	AI008985	n,o		ESTs
778	3278	AI008988	y,z	HHs:breakpoint cluster region	ESTs, Weakly similar to chimerin (chimaerin) 1 [Rattus norvegicus] [R.norvegicus]
779	16652	AI009019	b		ESTs, Moderately similar to EAR2_RAT Orphan nuclear receptor EAR-2 (V-erbA related protein EAR 2) (Ovalbumin upstream promoter gamma nuclear receptor rCOUPg) [R.norvegicus]
780	23337	AI009096	l,m	double-stranded RNA-binding protein p74	double-stranded RNA-binding protein p74
781	21632	AI009167	a,y,z,ee,ff		ESTs, Highly similar to BAG2_HUMAN BAG-family molecular chaperone regulator-2 [H.sapiens]
782	21596	AI009168	j,k		ESTs, Weakly similar to rhoB gene [Rattus norvegicus] [R.norvegicus]
783	22801	AI009197	e		ESTs, Moderately similar to hypothetical protein IMAGE3455200 [Homo sapiens] [H.sapiens]
784	9150	AI009198	h,i		ESTs, Highly similar to UNRI_MOUSE UNR-interacting protein (Serine-threonine kinase receptor associated protein) [M.musculus]
785	3755	AI009208	h,i		ESTs
786	7524	AI009350	d		ESTs, Weakly similar to C37H5.3.p [Caenorhabditis elegans] [C.elegans]
787	3979	AI009368	s,t		ESTs
788	10820	AI009411	g,h,i		ESTs, Highly similar to RS3_MOUSE 40S ribosomal protein S3 [R.norvegicus]
789	3836	AI009420	aa,bb	synaptic vesicle glycoprotein 2 b	synaptic vesicle glycoprotein 2 b
790	4154	AI009467	kk		ESTs
791	9746	AI009555	r		Rattus norvegicus dynein light intermediate chain 1 mRNA, complete cds
792	10532	AI009602	ii		ESTs
793	895	AI009614	h,i		ESTs
794	4168	AI009654	ll		ESTs
795	16154	AI009661	a		ESTs, Moderately similar to AF1Q_MOUSE Protein AF1Q [M.musculus]
796	19358	AI009675	b,c,v		EST
797	22464	AI009713	t		ESTs
798	22545	AI009747	a	transducer of ERBB2, 1	transducer of ERBB2, 1
799	15089	AI009752	gg		ESTs
800	6844	AI009770	j,k		ESTs
801	23092	AI009819	u,v		ESTs
802	2605	AI009843	j,k		ESTs
803	26133	AI009950	g		EST

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
804	18680	AI010084	l,m		ESTs
805	15988	AI010108	s,t		ESTs
806	4177	AI010123	aa,bb		ESTs
807	3316	AI010237	ii		ESTs
808	2612	AI010241	aa,bb		ESTs
809	15644	AI010256	kk	H3 histone, family 3B	H3 histone, family 3B
810	6897	AI010275	ll		ESTs
811	3271	AI010303	g		ESTs
812	15924	AI010312	l,m		ESTs
813	21825	AI010418	cc,dd		ESTs
814	19778	AI010455	w,x		ESTs, Weakly similar to DNA-directed RNA polymerase I like [Caenorhabditis elegans] [C.elegans]
815	17524	AI010568	jj,kk	Growth hormone receptor	Growth hormone receptor
816	6936	AI010593	t		ESTs
817	18691	AI010605	b		ESTs, Moderately similar to S63665 titin protein - human (fragment) [H.sapiens]
818	3211	AI010612	n,o,hh		ESTs
819	23857	AI010616	e		ESTs
820	3139	AI010618	ee,ff		ESTs
821	6946	AI010642	jj,kk,ll		ESTs
822	11227	AI010660	c		ESTs
823	17761	AI010662	c,r		ESTs, Highly similar to S37488 gene T10 protein - mouse [M.musculus]
824	6984	AI010848	f,g		ESTs
825	24089	AI010865	e,n,o		ESTs
826	11684	AI010917	a		ESTs
827	18438	AI010930	e,r	ribosomal protein L14	ribosomal protein L14
828	11424	AI010936	jj,kk		ESTs, Moderately similar to PTN3_HUMAN Protein tyrosine phosphatase, non-receptor type 3 (Protein-tyrosine phosphatase H1) (PTP-H1) [H.sapiens]
829	13296	AI011020	ll		ESTs, Moderately similar to MTM1_MOUSE Myotubularin [M.musculus]
830	5983	AI011070	aa,bb,gg		ESTs
5	22030	AI011177	h,i	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
831	13787	AI011462	cc,dd		ESTs, Highly similar to CU59_HUMAN Protein C21orf59 [H.sapiens]
832	24022	AI011474	a,ee,ff,ll		ESTs, Moderately similar to T00637 hypothetical protein H_GS541B18.1 - human (fragment) [H.sapiens]
833	15917	AI011498	b	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
834	7060	AI011547	b		ESTs, Highly similar to T47183 hypothetical protein DKFZp434K1822.1 - human (fragment) [H.sapiens]
835	3941	AI011598	t,kk		ESTs, Moderately similar to LMA5_MOUSE Laminin alpha-5 chain precursor [M.musculus]
836	4350	AI011644	e		ESTs
837	21468	AI011749	cc,dd		ESTs
838	2519	AI011770	y,z		ESTs
839	17830	AI011943	c	Hemoglobin, beta	Hemoglobin, beta
840	14625	AI011949	cc,dd		ESTs
841	2531	AI011991	n,o	Ras homolog gene family, member G	Ras homolog gene family, member G



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SEQ. ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
842	24038	AI012109	w,x		ESTs, Highly similar to LSP1_MOUSE Lymphocyte-specific proteins LSP1 and S37 (PP52 protein) (52 kDa phosphoprotein) (Lymphocyte-specific antigen WP34) (S37 protein) [M.musculus]
843	2341	AI012144	d		ESTs
844	13093	AI012177	h,l		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
845	14668	AI012185	bb		ESTs
846	11752	AI012208	jj,kk		ESTs
847	21796	AI012221	a,n,o,x,z,kk		ESTs, Weakly similar to intracellular chloride ion channel protein p64H1 [Rattus norvegicus] [R.norvegicus]
848	3932	AI012271	d		ESTs
849	6606	AI012308	a,n,o,x,hh,kk		ESTs
850	11408	AI012353	u,v		ESTs
851	24200	AI012356	j,k,gg		ESTs
852	7471	AI012379	p,q		ESTs
853	23385	AI012380	b		ESTs, Weakly similar to hypothetical protein 24432 [Homo sapiens] [H.sapiens]
854	7120	AI012393	v		ESTs, Weakly similar to JE0343 terf protein - rat [R.norvegicus]
855	2456	AI012423	ii		ESTs
856	22651	AI012434	e		ESTs
857	5595	AI012467	u,v		ESTs, Weakly similar to UBP2_MOUSE Ubiquitin carboxyl-terminal hydrolase 2 (Ubiquitin thiolesterase 2) (Ubiquitin-specific processing protease 2) (Deubiquitinating enzyme 2) (41 kDa ubiquitin-specific protease) [M.musculus]
858	3304	AI012471	jj,kk		ESTs, Weakly similar to Y48B6A.6.p [Caenorhabditis elegans] [C.elegans]
859	14431	AI012516	h,l		ESTs, Weakly similar to T47155 hypothetical protein DKFZp564B0982.1 - human [H.sapiens]
860	17489	AI012566	d	unconventional myosin Myr2 I heavy chain	unconventional myosin Myr2 I heavy chain
861	23025	AI012621	j,k		ESTs, Weakly similar to T00357 hypothetical protein KIAA0685 - human [H.sapiens]
862	6489	AI012636	ll		ESTs, Weakly similar to RBMA_RAT RNA-binding protein 10 (RNA binding motif protein 10) (S1-1 protein) [R.norvegicus]
863	7044	AI012641	l,m		ESTs, Highly similar to I48722 zinc finger protein - mouse (fragment) [M.musculus]
864	7171	AI012761	cc,dd		ESTs
865	20924	AI012832	ii,ll	stannin	stannin
866	4232	AI012958	w,x		ESTs
867	7193	AI013033	gg		ESTs
868	3191	AI013075	l,m		ESTs, Moderately similar to hypothetical protein FLJ14621 [Homo sapiens] [H.sapiens]
869	7220	AI013098	t		ESTs
870	16686	AI013160	u,v		ESTs, Weakly similar to I63168 gene Ube1x protein - rat (fragment) [R.norvegicus]
871	16984	AI013161	aa,bb		ESTs, Highly similar to EF1G_MOUSE Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) [M.musculus]
872	1332	AI013222	e	Platelet-derived growth factor A chain	ESTs, Platelet-derived growth factor A chain
873	20086	AI013260	z	lamin A	lamin A
874	3088	AI013369	bb		ESTs

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SEQ. ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
875	6758	AI013394	d,jj,kk	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
876	26148	AI013396	cc,dd		
877	19467	AI013397	ii		ESTs
878	23444	AI013448	d		ESTs, Highly similar to chromosome 20 open reading frame 30; HSPC274 protein [Homo sapiens] [H.sapiens]
879	22493	AI013466	cc,dd		ESTs, Moderately similar to KIAA1049 protein [Homo sapiens] [H.sapiens]
880	12233	AI013474	y,z,ee,ff		ESTs, Highly similar to HPS1_HUMAN Protein PHPS1-2 [H.sapiens]
881	1906	AI013477	gg		Rat VL30 element mRNA
882	12796	AI013495	u,v,cc,dd		ESTs, Weakly similar to R10D12.12.p [Caenorhabditis elegans] [C.elegans]
883	7264	AI013499	u,v		EST
884	9551	AI013558	t		ESTs
885	4253	AI013566	jj,kk		ESTs, Weakly similar to FIBB_RAT Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] [R.norvegicus]
886	3445	AI013724	e		ESTs, Weakly similar to T46337 hypothetical protein DKFZp434O2413.1 - human (fragment) [H.sapiens]
887	22592	AI013740	n,o,w,x		ESTs, Moderately similar to S32567 A4 protein - human [H.sapiens]
888	16584	AI013765	w,x	Arrestin, beta 2	Arrestin, beta 2
889	21950	AI013861	a,h,l	3-hydroxyisobutyrate dehydrogenase	3-hydroxyisobutyrate dehydrogenase
890	12802	AI013865	d		ESTs
891	2708	AI013882	r,y,z		ESTs, Highly similar to S53612 gene MSSP-2 protein - human [H.sapiens]
892	7299	AI013911	t		ESTs, Weakly similar to cold inducible RNA-binding protein [Rattus norvegicus] [R.norvegicus]
893	21604	AI013913	ii		ESTs
894	15786	AI013924	b,l,m		ESTs
895	15904	AI013971	l,m	neurofascin	neurofascin
896	7212	AI014065	gg		ESTs, Weakly similar to PMX1_MOUSE Paired mesoderm homeobox protein 1 (PRX-1) (Paired related homeobox protein 1) (Homeobox protein MhoX) (Homeobox protein K-2) (RhoX) [R.norvegicus]
897	15494	AI014094	s,t		ESTs, Weakly similar to DPSD_CAEEL Putative phosphatidylserine decarboxylase proenzyme [C.elegans]
6	19372	AI014135	h	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	beta-carotene 15, 15'-dioxygenase
6	1808	AI014135	e,u,v	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	beta-carotene 15, 15'-dioxygenase
898	15247	AI014169	aa,bb	upregulated by 1,25-dihydroxyvitamin D-3	upregulated by 1,25-dihydroxyvitamin D-3
899	7315	AI028831	j,k,kk		ESTs, Weakly similar to mitogen activated protein kinase kinase kinase 5; MEK kinase 5 [Mus musculus] [M.musculus]
900	16631	AI028856	j,k,y,z		ESTs
901	12805	AI028870	b,l,m,u,v		ESTs
902	3625	AI028954	ii		ESTs, Weakly similar to PT0194 protein-tyrosine kinase (EC 2.7.1.112) tyro-12 - rat (fragment) [R.norvegicus]

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
903	17957	AI028975	s,t	Adaptor protein complex AP-1, beta 1 subunit	Adaptor protein complex AP-1, beta 1 subunit
904	5422	AI028998	u,v		ESTs, Weakly similar to sequence-specific single-stranded-DNA-binding protein [Rattus norvegicus] [R.norvegicus]
905	11326	AI029015	ee,ff		ESTs
906	7362	AI029026	kk		ESTs
907	12387	AI029051	e		ESTs
908	9317	AI029174	a,jj,kk		ESTs
909	12662	AI029179	d,ee,ff,jj,kk,ll		ESTs
910	7447	AI029432	u,v		ESTs
911	12819	AI029437	jj,kk		ESTs
912	7451	AI029450	y,z		ESTs, Moderately similar to SYEP_HUMAN Bifunctional aminoacyl-tRNA synthetase [Includes: Glutamyl-tRNA synthetase (Glutamate-tRNA ligase); Prolyl-tRNA synthetase (Proline-tRNA ligase)] [H.sapiens]
913	7493	AI029608	y,z		ESTs
914	18885	AI029827	d		ESTs, Weakly similar to S46814 ribosomal protein YmS2, mitochondrial - yeast (Saccharomyces cerevisiae) [S.cerevisiae]
915	10650	AI029942	jj,kk		ESTs, Highly similar to CAV1_MOUSE Caveolin-1 [M.musculus]
916	10658	AI030028	e		ESTs
917	10665	AI030067	gg		ESTs
918	7615	AI030163	t		ESTs
919	10685	AI030213	cc,dd		ESTs
920	10690	AI030276	u,v		ESTs
921	6192	AI030301	gg		ESTs
922	665	AI030430	r		ESTs
923	10710	AI030494	ee,ff		ESTs
924	7698	AI030527	u,v		ESTs
925	7715	AI030599	l,m,ii		ESTs
926	7665	AI030668	a	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
927	7751	AI030750	p,q		ESTs
928	19257	AI030775	m		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
929	17013	AI030797	aa,bb		ESTs
930	7760	AI030806	kk		ESTs
931	17552	AI030833	u,v		ESTs
932	22614	AI031004	t		ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]
933	23950	AI031019	s,t	translation initiation factor eIF-2B alpha-subunit	translation initiation factor eIF-2B alpha-subunit
934	7842	AI031052	aa,bb		ESTs
935	7844	AI031058	h,l		ESTs, Highly similar to GDP-mannose pyrophosphorylase B, isoform 2; mannose-1-phosphate guanylyltransferase [Homo sapiens] [H.sapiens]
936	7846	AI031059	ll		ESTs
937	7852	AI043636	aa,bb,gg		ESTs
938	7867	AI043695	t	phosphoribosyl pyrophosphate amidotransferase	phosphoribosyl pyrophosphate amidotransferase
939	7880	AI043714	ii		ESTs, Weakly similar to T17271 hypothetical protein DKFZp434B0335.1 - human [H.sapiens]
940	7584	AI043724	gg		ESTs
941	18915	AI043798	f,g		ESTs
942	7903	AI043805	ii		ESTs

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
943	7913	AI043849	ee,ff		ESTs, Weakly similar to ELL_MOUSE RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) [M.musculus]
944	3899	AI043904	u,v		ESTs
945	6766	AI043914	h,l		ESTs
946	7961	AI044042	l,m		ESTs, Weakly similar to TC17_RAT Zinc finger protein 354A (Transcription factor 17) (Renal transcription factor Kid-1) (Kidney, ischemia, and developmentally regulated protein-1) [R.norvegicus]
947	5370	AI044087	u,v		EST
948	5371	AI044089	cc,dd		EST
949	19121	AI044101	gg		ESTs
950	5378	AI044112	l,m		ESTs
951	9838	AI044124	ii		ESTs
952	12778	AI044211	cc,dd		ESTs
953	5430	AI044253	d		EST
954	6745	AI044258	ii		ESTs
955	5433	AI044271	u,v		ESTs
956	5442	AI044299	y,z,ee,ff		ESTs
957	5454	AI044330	cc,dd		ESTs
958	5461	AI044338	a,y,z,kk		ESTs
959	5486	AI044397	gg		ESTs
960	5513	AI044521	ii		EST
961	6997	AI044539	c		ESTs
962	9876	AI044553	l,m		ESTs
963	5553	AI044632	l,m		ESTs
964	5710	AI044740	u,v		ESTs
965	5596	AI044747	g,kk		ESTs
966	2348	AI044794	j,k		ESTs
967	5322	AI044801	c		ESTs
968	7992	AI044845	cc,dd,gg		ESTs, Weakly similar to T12482 hypothetical protein DKFZp564P0662.1 - human (fragments) [H.sapiens]
969	9914	AI044855	aa,bb		ESTs
970	5615	AI044861	e		ESTs
971	6496	AI044887	u,v		ESTs
972	20983	AI044900	a,h,l,ee,ff,kk	fatty acid Coenzyme A ligase, long chain 2	fatty acid Coenzyme A ligase, long chain 2
973	5675	AI045026	j,k,p,q,ee,ff,kk		ESTs
974	24290	AI045040	cc,dd		ESTs, Weakly similar to T15251 hypothetical protein K07B1.4 - Caenorhabditis elegans [C.elegans]
975	5689	AI045075	d		ESTs, Weakly similar to Exonuclease [Caenorhabditis elegans] [C.elegans]
976	5726	AI045194	b,u,v		ESTs
977	5775	AI045378	ee,ff,gg		ESTs
978	5795	AI045441	ll		ESTs
979	16752	AI045475	d,jj,kk		ESTs
980	10004	AI045509	gg,ii		ESTs
981	6808	AI045600	w,x		ESTs, Highly similar to S30034 translocating chain-associating membrane protein - human [H.sapiens]
982	10020	AI045632	k,y,z		ESTs
983	2662	AI045686	e		ESTs, Weakly similar to CBP_MOUSE CREB-binding protein [M.musculus]
984	10028	AI045707	n,o		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
985	16335	AI045744	b,u,v	Solute carrier family 4, member 1, anion exchange protein 1 (kidney band 3)	Solute carrier family 4, member 1, anion exchange protein 1 (kidney band 3)
986	5890	AI045836	u,v		ESTs
987	2360	AI045911	cc,dd		ESTs
988	5913	AI045929	b		ESTs
989	10053	AI045948	n,o		ESTs
990	3319	AI045989	b,l,m		ESTs
991	8012	AI058330	ee,ff,kk	decay-accelarating factor	decay-accelarating factor
992	6828	AI058359	s,t		ESTs, Weakly similar to T46465 hypothetical protein DKFZp434A0530.1 - human [H.sapiens]
993	8039	AI058419	u,v,aa,bb		ESTs
994	6737	AI058451	u,v		ESTs
995	8627	AI058453	l,m		ESTs
996	10070	AI058505	u,v		EST, Weakly similar to RRM2_HUMAN Putative ribosomal RNA methyltransferase 2 (rRNA (uridine-2'-O-)-methyltransferase) [H.sapiens]
997	10072	AI058507	a		ESTs, Highly similar to Nedd4 WW binding# protein 4; Nedd4 WW-binding protein 4 [Mus musculus] [M.musculus]
998	8612	AI058527	v		ESTs
999	8103	AI058653	u,v		
1000	8110	AI058665	d		ESTs
1001	10096	AI058772	n,o		EST
1002	8158	AI058824	u,v		ESTs
1003	19093	AI058869	l,m		ESTs, Highly similar to SUI1_MOUSE Protein translation factor SUI1 homolog [M.musculus]
1004	10115	AI058890	r		ESTs
1005	5549	AI058942	u,v		ESTs
1006	8539	AI059175	e	pericentriolar material 1	pericentriolar material 1
1007	10171	AI059209	u,v		EST
1008	8265	AI059246	cc,dd		EST
1009	8285	AI059298	cc,dd		ESTs
1010	8290	AI059312	ee,ff		ESTs
1011	8291	AI059313	b		EST
1012	8303	AI059352	s,t		ESTs
1013	8314	AI059386	p,q		ESTs
1014	8729	AI059485	w,x		ESTs, Weakly similar to NCP1_RAT Nck-associated protein 1 (NAP 1) (p125Nap1) (Membrane-associated protein HEM-2) [R.norvegicus]
1015	8347	AI059519	n,o		ESTs, Weakly similar to EGRT epidermal growth factor precursor - rat [R.norvegicus]
1016	8356	AI059543	b		ESTs, Weakly similar to pseudouridylyl synthase; orf, hypothetical protein [Escherichia coli K12] [E.coli]
1017	7970	AI059549	l,m		ESTs
1018	10233	AI059664	ii		ESTs
1019	8423	AI059728	cc,dd		EST
1020	10277	AI059925	u,v		EST, Weakly similar to T42092 s-afadin - rat [R.norvegicus]
1021	8494	AI059968	a		ESTs
1022	8495	AI059971	a,t		ESTs, Weakly similar to 2205324A lymphotoxin beta receptor [Mus musculus] [M.musculus]
1023	10302	AI060137	cc,dd		EST
1024	8557	AI060221	u,v		ESTs
1025	8745	AI069939	t		ESTs
1026	17506	AI070068	p,q	HHs: growth arrest and DNA-damage-inducible, beta	ESTs, Weakly similar to 2104282A Gadd45 gene [Rattus norvegicus] [R.norvegicus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1027	2742	AI070173	a		ESTs
1028	4967	AI070179	w,x		ESTs, Highly similar to JC7218 glia maturation factor-gamma - rat [R.norvegicus]
1029	18	AI070195	w,x		ESTs, Highly similar to T42648 hypothetical protein DKFZp434C1415.1 - human [H.sapiens]
1030	17796	AI070214	l,m		ESTs
1031	8854	AI070285	aa,bb		ESTs
1032	21364	AI070392	b,u,v		ESTs
1033	23277	AI070508	ii		ESTs
1034	8938	AI070590	a,ee,ff,kk		ESTs
1035	8965	AI070660	gg		EST
1036	10453	AI070697	b,u,v		EST
1037	8980	AI070710	d		ESTs
1038	21195	AI070726	h,l		ESTs
1039	18598	AI070775	a		ESTs
1040	10345	AI071049	d		ESTs
1041	9554	AI071131	u,v		ESTs
1042	23437	AI071166	r		ESTs
1043	9579	AI071174	d		ESTs
1044	9583	AI071185	y,z,kk		ESTs
1045	11017	AI071222	c,r		ESTs
1046	9604	AI071230	ee,ff,gg		ESTs, Weakly similar to I48842 testin - mouse [M.musculus]
1047	11024	AI071285	ii		ESTs
1048	9649	AI071429	d		ESTs
1049	9668	AI071538	r		ESTs
1050	22929	AI071578	ee,ff,kk		ESTs, Moderately similar to S29993 P311 protein - mouse [M.musculus]
1050	22930	AI071578	g,jj,kk		ESTs, Moderately similar to S29993 P311 protein - mouse [M.musculus]
1051	8099	AI071586	gg		ESTs
1052	11086	AI071698	hh		ESTs
1053	11088	AI071703	p,q		ESTs
1054	8712	AI071935	b,u,v		ESTs, Highly similar to RIKEN cDNA 1110003N24 [Mus musculus] [M.musculus]
1055	9788	AI071958	b		ESTs
1056	8665	AI071965	ee,ff		ESTs, Moderately similar to T17342 hypothetical protein DKFZp586K1924.1 - human (fragment) [H.sapiens], R.norvegicus hsp70.2 mRNA for heat shock protein 70
1057	9801	AI072019	b		ESTs
1058	9806	AI072036	aa,bb		ESTs
1059	9808	AI072050	n,o		ESTs
1060	18198	AI072063	n,o		ESTs, Moderately similar to S11276 alpha-adaptin c - rat [R.norvegicus]
1061	9186	AI072088	b		ESTs
1062	5740	AI072092	l,m		ESTs, Highly similar to DYNC_HUMAN Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide) (Dynamitin) (DCTN-50) [H.sapiens]
1063	10837	AI072144	y,z,ee,ff		ESTs
1064	7516	AI072183	p,q		ESTs
1065	9218	AI072197	n,o		EST
1066	9305	AI072520	aa,bb		ESTs
1067	10900	AI072594	ii		EST
1068	6548	AI072658	a,t,kk,ll		ESTs
1069	10918	AI072733	r		EST
1070	9380	AI072738	d		ESTs
1071	10919	AI072744	h,l,w,x		ESTs

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1072	9408	AI072835	cc,dd		ESTs
1073	9409	AI072841	b		ESTs, Moderately similar to S69000 laminin gamma 2 chain - mouse [M.musculus]
1074	10930	AI072900	c		ESTs
1075	9454	AI072992	ll		ESTs
1076	9611	AI073040	a		ESTs
1077	9485	AI073109	ll		ESTs, Highly similar to BANP homolog; putative transcription factor; Btg3 associated nuclear protein [Mus musculus] [M.musculus]
1078	9466	AI073135	cc,dd		ESTs
1079	10970	AI073207	n,o		ESTs
1080	10971	AI073212	g,j,k		ESTs
1081	19371	AI100841	cc,dd		ESTs
1082	15192	AI101099	j,k		ESTs, Highly similar to SMRT2 metallothionein II - rat [R.norvegicus]
1083	7868	AI101229	jj,kk		ESTs
1084	5421	AI101270	aa,bb	HMm:Rho, GDP dissociation inhibitor (GDI) beta	ESTs, Highly similar to I49687 GDP-dissociation inhibitor - mouse [M.musculus]
1085	4027	AI101330	e		ESTs
1086	11634	AI101338	n,o		ESTs
1087	2292	AI101362	hh		ESTs
1088	18212	AI101494	cc,dd		ESTs
1089	6640	AI101500	e		ESTs
1090	22786	AI101659	gg		ESTs, Weakly similar to dual-specificity phosphatase [Mus musculus] [M.musculus]
1091	13267	AI101847	h,l	Potassium (K+) channel protein alpha 5	Potassium (K+) channel protein alpha 5
1092	4432	AI101851	t		ESTs
1093	2042	AI101921	s,t		ESTs
1094	11399	AI101924	r,jj,kk		ESTs
1095	11598	AI102007	h,l		ESTs
1096	3085	AI102046	c		ESTs
1097	3996	AI102061	r		ESTs
1098	10227	AI102248	kk		ESTs
1099	16596	AI102486	ee,ff,kk		ESTs, Weakly similar to S37583 RING finger protein rfp - mouse (fragment) [M.musculus]
1100	11953	AI102505	hh	cytochrome c oxidase, subunit VIIIa	cytochrome c oxidase, subunit VIIIa
1100	11954	AI102505	hh	cytochrome c oxidase, subunit VIIIa	cytochrome c oxidase, subunit VIIIa
1101	2125	AI102519	n,o,w,x		ESTs, Highly similar to TYRO protein tyrosine kinase binding protein; killer cell activating receptor associated protein [Mus musculus] [M.musculus]
1102	5969	AI102520	b,l,m,bb,kk		ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus]
1103	4102	AI102524	gg		ESTs, Highly similar to CBX2_MOUSE Chromobox protein homolog 2 (Modifier 3 protein) (M33) [M.musculus]
1104	11563	AI102560	b,e,l,m		ESTs
1105	22487	AI102578	e		ESTs, Highly similar to I49523 tumor necrosis factor alpha-induced protein 2 - mouse [M.musculus]
1106	19011	AI102618	p,q		ESTs
1107	19379	AI102711	w,x		ESTs, Highly similar to RIKEN cDNA 061001012 [Mus musculus] [M.musculus]
1108	22171	AI102734	w,x		ESTs, Moderately similar to JC4965 elk1 protein - mouse [M.musculus]
1109	5891	AI102745	cc,dd		ESTs

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1110	11724	AI102812	c		ESTs
1111	18916	AI102819	e		ESTs
1112	11723	AI102896	aa,bb		ESTs
1113	24229	AI102972	r		ESTs
1114	10659	AI103059	j,k		ESTs
1115	8124	AI103071	s,t,li		ESTs
1116	2316	AI103084	hh		ESTs, Moderately similar to selective hybridizing clone [Mus musculus] [M.musculus]
1117	3584	AI103106	r		ESTs
1118	17642	AI103357	cc,dd		ESTs
1119	11721	AI103391	ee,ff		ESTs, Highly similar to phosphatidylinositol 3-kinase, regulatory subunit, polypeptide [Rattus norvegicus] [R.norvegicus]
7	14980	AI103396	l,m	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	Rattus norvegicus CDK110 mRNA
7	14981	AI103396	e	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	Rattus norvegicus CDK110 mRNA
1120	3905	AI103403	a	polypyrimidine tract binding protein	polypyrimidine tract binding protein
1121	15841	AI103465	t		ESTs, Moderately similar to RP29_HUMAN Ribonuclease P protein subunit p29 [H.sapiens]
1122	4873	AI103531	l,m,ee,ff		ESTs, Highly similar to toll-associated serine protease [Mus musculus] [M.musculus]
1123	7528	AI103548	r		ESTs, Moderately similar to T24634 hypothetical protein T07C4.10b - Caenorhabditis elegans [C.elegans]
1124	21579	AI103572	p,q		ESTs
1125	15942	AI103738	h,l		ESTs
1126	17762	AI103854	c		ESTs, Highly similar to S37488 gene T10 protein - mouse [M.musculus]
1127	4402	AI103874	r		ESTs, Weakly similar to FKBP1_RAT FK506-BINDING PROTEIN (FKBP-12) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIASE) (ROTAMASE) (IMMUNOPHILIN FKBP12) [R.norvegicus]
1128	11516	AI103962	dd		ESTs
1129	16136	AI103983	p,q	unknown Glu-Pro dipeptide repeat protein	unknown Glu-Pro dipeptide repeat protein
1130	26213	AI104113	f,g		
1131	21927	AI104117	w,x		Rattus norvegicus LIM-domain protein LMP-1 mRNA, complete cds
1132	8458	AI104239	gg		ESTs
1133	3527	AI104278	n,o		ESTs
1134	11522	AI104303	y,z		ESTs
1135	15416	AI104340	d		ESTs
1136	2856	AI104349	d		ESTs
1137	18831	AI104357	bb		ESTs, Highly similar to ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin) [R.norvegicus]
1138	23574	AI104520	hh	Cytochrome c oxidase subunit VIa (liver)	Cytochrome c oxidase subunit VIa (liver)
1139	18509	AI104528	hh		ESTs, Weakly similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17) [Homo sapiens] [H.sapiens]
1140	4782	AI104570	r		ESTs
1141	11680	AI104605	jj,kk		ESTs
1142	4626	AI104744	j,k,l,m		ESTs
1143	14464	AI104848	kk		ESTs



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1144	6205	AI104907	g	TEMO	TEMO
1145	8273	AI104908	ii		ESTs
1146	24375	AI104979	j,k		ESTs, Moderately similar to EBNA1 binding protein 2; nucleolar protein p40; homolog of yeast EBNA1-binding protein; nuclear FGF3 binding protein; EBNA1-binding protein 2 [Homo sapiens] [H.sapiens]
1147	3802	AI105044	gg		Rattus norvegicus 250 kDa estrous-specific protein mRNA, partial cds
1148	21361	AI105161	d		ESTs
1149	2196	AI105243	jj,kk		ESTs
1150	23596	AI105435	bb	HHs:glutaryl-Coenzyme A dehydrogenase	ESTs, Highly similar to GCDH_MOUSE Glutaryl-CoA dehydrogenase, mitochondrial precursor (GCD) [M.musculus]
1151	15197	AI105444	d,kk		ESTs
1152	15291	AI111401	hh	multiple inositol polyphosphate histidine phosphatase 1	multiple inositol polyphosphate histidine phosphatase 1
1153	4479	AI111599	j,k,jj,kk		ESTs
1154	18439	AI111877	r	ribosomal protein L14	ribosomal protein L14
1155	2539	AI111960	e,kk		ESTs, Weakly similar to FKB5_MOUSE 51 kDa FK506-binding protein (FKBP51) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) [M.musculus]
1156	12887	AI112095	hh		ESTs, Highly similar to JC5556 adhalin - mouse [M.musculus]
1157	4143	AI112107	gg		ESTs
1158	14434	AI112291	ll		ESTs, Weakly similar to T46612 multi PDZ domain protein 1 - rat [R.norvegicus]
1159	22744	AI112512	h,l		ESTs
1160	12969	AI112969	p,q		ESTs
1161	2296	AI112979	w,x		ESTs, Highly similar to SAP3_MOUSE Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator protein 3) (SAP-3) [M.musculus]
1162	4969	AI113008	l,k,n,o		ESTs, Weakly similar to vitronectin [Rattus norvegicus] [R.norvegicus]
1163	23428	AI113320	ll		ESTs, Moderately similar to JC4365 arginine-tRNA ligase (EC 6.1.1.19) - human [H.sapiens]
1164	6166	AI136516	r,kk		ESTs
1165	21019	AI136547	y,z		ESTs
1166	10780	AI136555	c		Rattus norvegicus mRNA for Castration Induced Prostatic Apoptosis Related protein-1 (CIPAR-1)
1167	24212	AI136747	cc,dd		ESTs, Highly similar to H33_HUMAN Histone H3.3 (H3.A) (H3.B) (H3.3Q) [M.musculus]
1168	13080	AI136842	e		ESTs
1169	13082	AI136848	c		ESTs, Weakly similar to T34013 hypothetical protein Y4C6B.5 - Caenorhabditis elegans [C.elegans]
1170	13090	AI136977	cc,dd		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
1171	12878	AI137114	hh		ESTs
1172	13717	AI137131	n,o		ESTs, Moderately similar to S21976 probable RNA-directed DNA polymerase (EC 2.7.7.49) (clone MH2C) - rat retrotransposon L1 (fragment) [R.norvegicus]
1173	13291	AI137286	ee,ff		ESTs
1174	15969	AI137302	cc,dd		ESTs, Weakly similar to ZF37_RAT Zinc finger protein 37 (Zfp-37) [R.norvegicus]

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1175	9166	AI137406	kk		ESTs, Moderately similar to A55945 endothelial cell protein C receptor precursor - mouse [M.musculus]
1176	11238	AI137410	ee,ff		ESTs, Moderately similar to hypothetical protein FLJ12888 [Homo sapiens] [H.sapiens]
1177	7122	AI137468	gg		ESTs, Weakly similar to GPV_RAT Platelet glycoprotein V precursor (GPV) (CD42D) [R.norvegicus]
1178	18943	AI137495	d		ESTs, Highly similar to H2A1_RAT Histone H2A.1 [R.norvegicus]
1179	17402	AI137553	ee,ff	Transforming growth factor beta stimulated clone 22	Transforming growth factor beta stimulated clone 22
1180	6638	AI137579	bb		ESTs
1181	7414	AI137586	a		ESTs, Highly similar to IMB3_HUMAN Importin beta 3 subunit (Karyopherin beta-3 subunit) (Ran-binding protein 5) [H.sapiens]
1182	12654	AI137864	cc,dd		ESTs, Highly similar to MG15_HUMAN Transcription factor-like protein MRG15 (MORF-related gene 15 protein) (MSL3-1 protein) (Protein HSPC008/HSPC061) [H.sapiens]
1183	13227	AI137925	hh		ESTs
1184	12356	AI137931	l,m		ESTs
1185	23687	AI137958	g		ESTs
1186	14524	AI137974	d		ESTs, Highly similar to I57019 H3 histone - rat [R.norvegicus]
1187	11372	AI137995	c		ESTs
1188	13161	AI138093	g		ESTs
1189	13181	AI144948	r		ESTs
1190	6364	AI145058	gg		ESTs
1191	14458	AI145095	kk		ESTs
1192	13786	AI145106	hh		ESTs
1193	18206	AI145282	a,jj,kk		ESTs, Weakly similar to NUCL_RAT Nucleolin (Protein C23) [R.norvegicus]
1194	5732	AI145362	ll		ESTs
1195	13375	AI145454	cc,dd		ESTs
1196	11331	AI145556	t		ESTs
1197	23631	AI145650	j,k		ESTs
1198	8339	AI145761	w,x		ESTs, Weakly similar to T21659 hypothetical protein F32D8.4 - Caenorhabditis elegans [C.elegans]
1199	5531	AI145859	t		ESTs
1200	11337	AI145968	l,m		ESTs, Highly similar to RB6K_MOUSE Rabkinesin-6 (RAB6-interacting kinesin-like protein) (Kinesin-like protein 174) [M.musculus]
1201	11346	AI145991	jj,kk		ESTs, Highly similar to T46266 hypothetical protein DKFZp761A179.1 - human (fragment) [H.sapiens]
1202	11363	AI145997	hh		ESTs, Moderately similar to 2206377B MHR23B gene [Mus musculus] [M.musculus]
1203	18472	AI168975	j,k		ESTs, Weakly similar to Yeast hypothetical 52.9 KD protein like [Caenorhabditis elegans] [C.elegans]
1203	18473	AI168975	j,k,kk,ll		ESTs, Weakly similar to Yeast hypothetical 52.9 KD protein like [Caenorhabditis elegans] [C.elegans]
1204	21523	AI169104	e		ESTs, Highly similar to A26774 platelet factor 4 precursor - rat [R.norvegicus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1205	17914	AI169159	hh	HMm:ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E	ESTs, Moderately similar to VATE_MOUSE Vacuolar ATP synthase subunit E (V-ATPase E subunit) (Vacuolar proton pump E subunit) (V-ATPase 31 kDa subunit) (P31) [M.musculus]
1206	23152	AI169170	r	HHs:eukaryotic translation initiation factor 4A, isoform 2	ESTs, Highly similar to S00985 translation initiation factor eIF-4A II - mouse [M.musculus]
1207	12979	AI169177	a,p,q,y,z		ESTs, Highly similar to S33363 gly96 protein - mouse [M.musculus]
1208	2607	AI169211	r		ESTs, Highly similar to A47318 RNA-binding protein Raly - mouse [M.musculus]
1209	22661	AI169265	gg	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1
1210	149	AI169272	cc,dd		ESTs
1211	13240	AI169311	j,k		ESTs
1212	14525	AI169512	d		ESTs
1213	11550	AI169591	r		ESTs, Highly similar to S57447 HPBR11-7 protein - human [H.sapiens]
1214	4480	AI169601	hh		ESTs
1215	6888	AI169615	s,t	vesicle-associated membrane protein, associated protein A (33 kDa)	vesicle-associated membrane protein, associated protein A (33 kDa)
1216	23110	AI169640	t		ESTs, Highly similar to chromosome 11 hypothetical protein ORF3 [Homo sapiens] [H.sapiens]
1217	24146	AI169668	ii		ESTs, Weakly similar to ATP-binding cassette, sub-family F, member 2 [Homo sapiens] [H.sapiens]
1218	21660	AI169751	a,kk		Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
1219	804	AI169756	j,k,p,q		ESTs, Highly similar to G33_RAT GENE 33 POLYPEPTIDE [R.norvegicus]
1220	13427	AI169993	aa,bb		ESTs
1221	21185	AI170056	a		ESTs
1222	21254	AI170059	d		ESTs
1223	6969	AI170244	hh		ESTs, Moderately similar to g1-related zinc finger protein [Mus musculus] [M.musculus]
1224	22942	AI170251	aa,bb		ESTs
1225	3547	AI170279	ii		ESTs, Weakly similar to S54303 zinc transport protein ZnT-1 - rat [R.norvegicus]
1226	3486	AI170313	gg		ESTs
1227	2729	AI170363	e,j,k,t,ee,ff		ESTs
1228	5297	AI170379	a,p,q,y,z		ESTs
1229	22707	AI170384	cc,dd		ESTs
1230	16916	AI170406	h,l		ESTs
1231	18744	AI170407	d,kk		ESTs
1232	11585	AI170502	r	HMm:glycogen synthase 3, brain	ESTs, Weakly similar to A35362 UDPglucose--glycogen glucosyltransferase (EC 2.4.1.11), hepatic - rat [R.norvegicus]
1233	18811	AI170525	ii		ESTs
1234	16689	AI170561	cc,dd		ESTs
1235	2534	AI170632	aa,bb,ii		ESTs
1236	15393	AI170663	cc,dd	HHs:sterol regulatory element binding transcription factor 2	ESTs, Weakly similar to A48085 transcription factor ADD1 - rat [R.norvegicus]
1237	13365	AI170676	ee,ff		ESTs
1238	3973	AI170687	hh		ESTs
1239	6982	AI170793	kk		ESTs, Weakly similar to DCC_MOUSE Tumor suppressor protein DCC precursor [M.musculus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1240	21284	AI170842	hh		ESTs, Weakly similar to A57291 cytokine inducible nuclear protein C193 - human [H.sapiens]
1241	12695	AI170948	q		ESTs, Moderately similar to A57641 G protein-coupled receptor 4 - human [H.sapiens]
1242	7011	AI171019	aa,bb		ESTs
1243	13702	AI171064	n,o		ESTs
1244	22033	AI171165	aa,bb		ESTs
1245	17783	AI171206	ee,ff		ESTs, Weakly similar to 2118320A neurodegeneration-associated protein 1 [Rattus norvegicus] [R.norvegicus]
1246	21771	AI171209	n,o		ESTs
1247	5953	AI171231	s,t	amino acid transporter system A2	amino acid transporter system A2
1248	22432	AI171263	a,z		ESTs, Highly similar to S38342 fibrillarin - mouse [M.musculus]
1249	11426	AI171305	a,jj,kk		ESTs, Moderately similar to PTN3_HUMAN Protein tyrosine phosphatase, non-receptor type 3 (Protein-tyrosine phosphatase H1) (PTP-H1) [H.sapiens]
1250	14960	AI171319	w,x	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	ESTs, Highly similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1; integrase interactor 1 [Mus musculus] [M.musculus], guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
1251	14117	AI171350	e,p,q		ESTs
1252	18047	AI171359	bb		ESTs, Weakly similar to DnaJ-like protein [Rattus norvegicus] [R.norvegicus]
1253	16599	AI171366	ee,ff,jj,kk		ESTs, Weakly similar to S37583 RING finger protein rfp - mouse (fragment) [M.musculus]
1254	22958	AI171374	p,q,t		ESTs, Moderately similar to MEA6_HUMAN Meningioma-expressed antigen 6/11 (MEA6) (MEA11) [H.sapiens]
1255	17529	AI171460	h,i		ESTs, Weakly similar to HCD2_RAT 3-hydroxyacyl-CoA dehydrogenase type II (Type II HADH) (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) [R.norvegicus]
1256	13453	AI171518	r		ESTs
1257	17220	AI171521	c		ESTs
1258	11761	AI171526	d		ESTs
1259	5292	AI171607	t		ESTs
1260	6667	AI171646	gg		ESTs
1261	2795	AI171655	e		ESTs
1262	11696	AI171774	jj,kk		ESTs, Weakly similar to TMOD_MOUSE Tropomodulin [M.musculus]
1263	15449	AI171799	jj,kk		ESTs
1264	4420	AI171916	a,z		ESTs
1265	24220	AI171978	r		ESTs
1266	22239	AI171982	e		ESTs, Moderately similar to I48672 p8 MTCP-1 - mouse [M.musculus]
1267	6645	AI171998	jj,kk		ESTs
1268	1506	AI172051	n,o		ESTs, Highly similar to A29440 signal recognition particle receptor - human [H.sapiens]
1269	19012	AI172056	p,q,gg		ESTs
1270	9538	AI172097	l,m	heat shock transcription factor 1	heat shock transcription factor 1
1271	12367	AI172126	gg		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1272	16293	AI172183	c		ESTs, Weakly similar to RTN1_RAT Reticulon 1 (Neuroendocrine-specific protein) (S-rex) [R.norvegicus]
1273	6974	AI172263	d,r		ESTs
1274	23703	AI172265	cc,dd		ESTs
1275	23313	AI172271	r		ESTs
1276	2140	AI172272	hh		ESTs, Weakly similar to A53004 transcription elongation factor S-II - rat [R.norvegicus]
1277	24268	AI172281	g		ESTs
1278	1287	AI172299	kk		ESTs
1279	4278	AI172304	e	HMm:interleukin 2 receptor, gamma chain	ESTs, Highly similar to I49280 interleukin-2 receptor gamma chain precursor - mouse [M.musculus]
1280	11702	AI172305	e		ESTs
1281	13266	AI172326	j,k,ii		ESTs
1282	23390	AI172328	e	RNA binding protein p45AUF1	RNA binding protein p45AUF1
1283	12117	AI172352	hh,jj,kk		ESTs
1284	24209	AI172423	a,h,l,o,hh		ESTs
1285	2208	AI172472	cc,dd		ESTs, Weakly similar to HCCA2 protein [Homo sapiens] [H.sapiens]
1286	17291	AI172491	gg		ESTs, Weakly similar to A54756 isocitrate dehydrogenase (NADP+) (EC 1.1.1.42), cytosolic - rat [R.norvegicus]
1287	12043	AI172567	ii		ESTs
1288	13070	AI172569	h,l		EST
1289	11897	AI172598	jj,kk		ESTs
1290	11173	AI175005	r		ESTs
1291	7740	AI175011	r,hh		ESTs, Moderately similar to COF1_RAT COFILIN, NON-MUSCLE ISOFORM [R.norvegicus]
1292	17679	AI175025	hh		ESTs, Moderately similar to WS3_HUMAN WS-3 PROTEIN [H.sapiens]
1293	8053	AI175033	p,q		ESTs
1294	2331	AI175045	j,k,p,q,ee,ff,jj,k		ESTs
1295	3982	AI175100	h,l,kk,ll		ESTs
1296	19118	AI175281	hh	Guanidinoacetate methyltransferase	Guanidinoacetate methyltransferase
1297	21252	AI175328	n,o		ESTs, Weakly similar to S08464 T-cell alloantigen RT6.1 - rat [R.norvegicus]
1298	2448	AI175348	jj,kk		ESTs
1299	13460	AI175375	a,y,z,ee,ff,kk		ESTs
1300	4445	AI175466	r		ESTs, Weakly similar to RASH_RAT TRANSFORMING PROTEIN P21/H-RAS-1 (C-H-RAS) [R.norvegicus]
1301	13353	AI175508	j,k		ESTs
1302	18507	AI175551	h,l,w,x,kk		ESTs, Highly similar to EF1B_MOUSE Elongation factor 1-beta (EF-1-beta) [M.musculus]
1303	9979	AI175594	ii		ESTs
1304	2261	AI175619	ii		ESTs, Weakly similar to A53237 I(3)S12 protein - fruit fly (Drosophila melanogaster) (fragment) [D.melanogaster]
1305	15984	AI175777	j,k		ESTs
1306	19004	AI175875	aa,bb		Rattus norvegicus Sprague-Dawley lipid-binding protein mRNA, complete cds
1306	19005	AI175875	ii		Rattus norvegicus Sprague-Dawley lipid-binding protein mRNA, complete cds
1307	21755	AI175977	r		ESTs
1308	4074	AI175990	a,x		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1309	22451	AI175992	r		ESTs, Highly similar to beta-catenin-interacting protein ICAT [Mus musculus] [M.musculus]
1310	2046	AI176004	f,g		ESTs
1311	22311	AI176007	y,z		ESTs, Highly similar to PM5P_HUMAN Protein pM5 precursor [H.sapiens]
1312	12298	AI176055	aa,bb		ESTs
1313	5876	AI176117	hh	HMm:pyruvate dehydrogenase (lipoamide) beta	ESTs, ESTs, Highly similar to S15892 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - rat [R.norvegicus]
1314	4585	AI176121	f,g		ESTs
1315	6686	AI176130	d,jj,kk		ESTs
1316	17223	AI176140	r		ESTs, Highly similar to testis expressed gene 189 [Mus musculus] [M.musculus]
1317	18581	AI176160	n,o		ESTs
1318	6782	AI176170	e	FK506-binding protein 1 (12kD)	FK506-binding protein 1 (12kD)
1319	10182	AI176185	p,q,gg	FBJ murine osteosarcoma viral (v-fos) oncogene homolog	FBJ murine osteosarcoma viral (v-fos) oncogene homolog
1320	22765	AI176265	j,k,p,q,kk		ESTs
1321	12999	AI176276	h,i,p,q,y,z,gg		ESTs, Highly similar to UAP1_HUMAN UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Sperm-associated antigen 2) [Includes: UDP-N-acetylgalactosamine pyrophosphorylase (AGX-1); UDP-N-acetylglucosamine pyrophosphorylase (AGX-2)] [H.sapiens]
1322	16438	AI176294	cc,dd		ESTs, Highly similar to B Chain B, Crystal Structure Of The D1d2 Sub-Complex From The Human Snrnp Core Domain [H.sapiens]
1323	13339	AI176308	s,t		ESTs, Weakly similar to CO1B_RAT Coronin 1B (Coronin 2) [R.norvegicus]
1324	13511	AI176331	l,m		ESTs
1325	13504	AI176354	gg		ESTs, Weakly similar to YQT3_CAEEL HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN CHROMOSOME III [C.elegans]
1326	3014	AI176362	a,y,z,bb,kk,ll		ESTs
1327	19006	AI176393	aa,bb,ll		Rattus norvegicus Sprague-Dawley lipid-binding protein mRNA, complete cds
1328	17920	AI176422	ll		ESTs, Highly similar to S41115 probable flavoprotein-ubiquinone oxidoreductase (EC 1.6.5.-) - human [H.sapiens]
1329	24314	AI176434	hh		ESTs
1330	15191	AI176456	h,i,j,k,y,z,ee,ff,kk		ESTs, Highly similar to SMRT2 metallothionein II - rat [R.norvegicus]
1331	24763	AI176488	jj,kk	nuclear factor I/B	nuclear factor I/B
1332	22716	AI176500	f,g		ESTs, Highly similar to NIDO_RAT NIDOGEN (ENTACTIN) [R.norvegicus]
1333	8609	AI176505	hh		ESTs
1334	15959	AI176540	d,r		ESTs
1335	16518	AI176546	d,ee,ff,jj,kk	HMm:heat shock protein, 86 kDa 1	ESTs, Moderately similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
1336	5507	AI176584	c		Rattus norvegicus insulin-like growth factor binding protein 5 mRNA, 3' UTR
1337	3619	AI176588	j,k		ESTs, Weakly similar to tumor protein p53-binding protein; topoisomerase I binding protein [Homo sapiens] [H.sapiens]
1338	18525	AI176792	d		ESTs
1339	21740	AI176810	e,j,k,kk		ESTs
1340	6821	AI176841	ii		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1341	16917	AI176951	h,l		ESTs
1342	10310	AI176961	n,o	ribosomal protein, mitochondrial, L12	ribosomal protein, mitochondrial, L12
1343	16124	AI176963	p,q,r,bb,ee,ff,jj, kk	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
1344	7292	AI176995	c		ESTs, Moderately similar to T13963 formin related protein, lymphocyte specific - mouse [M.musculus]
1345	16493	AI177049	d		ESTs
1346	3969	AI177055	ii		ESTs
1347	2852	AI177059	c,g,kk		ESTs
1348	22077	AI177099	hh		ESTs
1349	5943	AI177105	j,k		ESTs, Weakly similar to OAF_DROME Out at first protein [Contains: Out at first short protein] [D.melanogaster]
1350	13310	AI177119	kk		ESTs, Weakly similar to S49158 complement protein C1q beta chain precursor - rat [R.norvegicus]
1351	12582	AI177183	c		ESTs
1352	7163	AI177256	h,l		ESTs
1353	13539	AI177280	w,x		ESTs, Weakly similar to GMCR_MOUSE Granulocyte-macrophage colony-stimulating factor receptor alpha chain precursor (GM-CSF-R-alpha) (GMR) [M.musculus]
1354	21785	AI177312	a		ESTs
1355	26254	AI177357	r		
1356	14989	AI177366	f,g,i,m,kk	Integrin, beta 1	Integrin, beta 1
1357	17826	AI177403	w,x		ESTs, Weakly similar to KLR6_MOUSE Killer cell lectin-like receptor 6 (T-cell surface glycoprotein LY-49F) (LY49-F antigen) [M.musculus]
1358	24129	AI177590	b		ESTs, Highly similar to T08750 hypothetical protein DKFZp586E1519.1 - human (fragment) [H.sapiens]
1359	17570	AI177683	n,o,hh		Rattus norvegicus mRNA for hnRNP protein, partial
1360	9521	AI177706	b,u,v		ESTs
1361	6562	AI177734	t		ESTs
1362	6334	AI177765	b		ESTs, Weakly similar to T20254 hypothetical protein C55A6.1 - Caenorhabditis elegans [C.elegans]
1363	22882	AI177804	aa,bb		ESTs, Moderately similar to acid sphingomyelinase-like phosphodiesterase 3a [Mus musculus] [M.musculus]
1364	11791	AI177843	aa,bb		ESTs, Highly similar to SAS_HUMAN Sarcoma amplified sequence [H.sapiens]
1365	547	AI177871	gg		ESTs, Highly similar to CDK1_MOUSE Cyclin-dependent kinase 2-associated protein 1 (CDK2-associated protein 1) (Putative oral cancer suppressor) (Deleted in oral cancer-1) (DOC-1) [M.musculus]
1366	15315	AI177911	h,l	calpactin I heavy chain	calpactin I heavy chain
1367	5929	AI177962	hh		ESTs, Moderately similar to S23251 protein-tyrosine kinase (EC 2.7.1.112) ark precursor - mouse [M.musculus]
1368	22691	AI177967	r,aa,bb		ESTs, Weakly similar to transforming growth factor-beta (TGF-beta) masking protein large subunit [Rattus norvegicus] [R.norvegicus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1369	19184	AI178025	p,q,kk		ESTs, Highly similar to TGIF_MOUSE 5'-TG-3' INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF) [M.musculus]
1370	17320	AI178069	kk		ESTs
1371	17847	AI178214	hh		ESTs
1372	23929	AI178222	ii		ESTs
1373	6059	AI178245	c		ESTs, Moderately similar to T13963 formin related protein, lymphocyte specific - mouse [M.musculus]
1374	4073	AI178272	hh		ESTs, Weakly similar to S51973 hypothetical protein YAL046c - yeast (Saccharomyces cerevisiae) [S.cerevisiae]
1375	3740	AI178277	d		ESTs
1376	6502	AI178283	r	HMm:phenylalanine-tRNA synthetase-like	ESTs, Highly similar to SYFB_MOUSE Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS) [M.musculus]
1377	5760	AI178361	n,o		ESTs
1378	2479	AI178384	hh		ESTs
1379	8445	AI178394	c		ESTs
1380	22197	AI178527	a,y,z		ESTs
1381	21311	AI178688	s,t		ESTs
1382	14530	AI178738	b		ESTs
1383	15091	AI178740	cc,dd		ESTs, Highly similar to A56418 transcription factor delta - mouse [M.musculus]
1384	23567	AI178746	p,q,y,z		ESTs
1385	16668	AI178751	ii	sialyltransferase 5	sialyltransferase 5
1386	18848	AI178816	n,o	eukaryotic translation initiation factor 4E	eukaryotic translation initiation factor 4E
1387	13592	AI178914	ii		ESTs, Weakly similar to T23419 hypothetical protein K07F5.14 - Caenorhabditis elegans [C.elegans]
1388	23043	AI178968	b		ESTs, Weakly similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus]
1389	18907	AI178971	c,v	Hemoglobin, alpha 1	Hemoglobin, alpha 1
1390	17358	AI179147	g		ESTs, Highly similar to B Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution [H.sapiens]
8	14983	AI179150	bb,cc,dd	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	Rattus norvegicus CDK110 mRNA
1391	8477	AI179167	j,k,y,z		ESTs
1392	4080	AI179227	ii		ESTs
1393	11242	AI179260	kk		ESTs
1394	7213	AI179356	w,x	plysia ras-related homolog A2	plysia ras-related homolog A2
1395	4188	AI179366	ee,ff		ESTs
1396	12011	AI179380	c		ESTs, Highly similar to open reading frame 12 [Mus musculus] [M.musculus]
1397	19783	AI179388	f,g		ESTs, Highly similar to RIKEN cDNA 0610040D20 [Mus musculus] [M.musculus]
1398	13029	AI179391	e,t,kk		ESTs
1399	15438	AI179399	e,g	collagen type V, alpha 2	collagen type V, alpha 2
1400	15042	AI179422	a,j,k		ESTs
1401	13619	AI179464	j,k		ESTs
1402	16081	AI179610	a,p,q,r,y,z,gg,k	Heme oxygenase	Heme oxygenase
1403	3094	AI179700	b,l,m		ESTs, Weakly similar to AGRT agrin - rat [R.norvegicus]
1404	6251	AI179854	ii		ESTs



TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1405	18895	AI179916	b,l,m		ESTs, Highly similar to HSPC038 protein [Homo sapiens] [H.sapiens]
1406	1686	AI179971	c	Hemoglobin, alpha 1	Hemoglobin, alpha 1
1406	1687	AI179971	b,c,v	Hemoglobin, alpha 1	Hemoglobin, alpha 1
1407	6455	AI179984	aa,bb		ESTs, Weakly similar to CPI3_RAT CONTRAPSIN-LIKE PROTEASE INHIBITOR 3 PRECURSOR (CPI-23) (SERINE PROTEASE INHIBITOR 1) (SPI-1) [R.norvegicus]
1408	15892	AI179988	j,k,kk		ESTs
1409	4189	AI180081	cc,dd		ESTs
1410	19828	AI180087	d		ESTs, Weakly similar to OZF_RAT Zinc finger protein OZF (POZF-1) [R.norvegicus]
1411	24028	AI180239	kk		ESTs
1412	5482	AI180252	e,r		ESTs
1413	17089	AI180281	b,l,m		ESTs, Moderately similar to JC4978 oxidative stress protein A170 - mouse [M.musculus]
1414	3352	AI180334	b,u,v		ESTs
1415	8180	AI180353	hh		ESTs, Weakly similar to LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus]
1416	14337	AI180414	b,c,l,m		ESTs, Weakly similar to T14106 probable GTPase-activating protein SPA-1 - rat [R.norvegicus]
1417	7117	AI227612	il		ESTs
1418	13664	AI227639	ll		ESTs
1419	1377	AI227715	a,ee,ff	Retinoblastoma-related gene	Retinoblastoma-related gene
1420	23015	AI227724	l,s,t,ll		ESTs
1421	2055	AI227751	ii		ESTs
1422	13673	AI227763	gg		ESTs, Highly similar to S26650 DNA-binding protein 5 - human [H.sapiens]
1423	22845	AI227887	e,aa,bb	cell division cycle 42	cell division cycle 42
1424	19474	AI227961	c,ii		EST
1425	8109	AI228147	gg		ESTs
1426	6715	AI228284	j,k		ESTs
1427	12946	AI228291	a,ee,ff,kk,ll		ESTs
1428	22915	AI228299	bb		ESTs, Highly similar to craniofacial development protein 1 [Mus musculus] [M.musculus]
1429	8917	AI228301	ee,ff,jj,kk		ESTs
1430	6102	AI228335	ee,ff		ESTs
1431	17892	AI228438	b,v		ESTs
1432	13741	AI228462	cc,dd		ESTs
1433	1473	AI228548	aa		ESTs, Highly similar to S10A_RAT S-100 protein, alpha chain [R.norvegicus]
1434	16053	AI228596	a,p,q,y,z,ee,ff		ESTs, Weakly similar to T16757 hypothetical protein R144.3 - Caenorhabditis elegans [C.elegans]
1435	3557	AI228672	gg		ESTs
1436	13270	AI228760	t		ESTs
1437	15078	AI228830	j,k	stearoyl-Coenzyme A desaturase 2	Rat DNA polymerase alpha mRNA, 3' end, stearoyl-Coenzyme A desaturase 2
1438	2210	AI228963	hh		ESTs, Weakly similar to T26088 hypothetical protein W02B12.7 - Caenorhabditis elegans [C.elegans]
1439	16203	AI229196	w,x,cc,dd	Synaptobrevin 1, Vesicle-associated membrane protein (synaptobrevin 2)	Synaptobrevin 1, Vesicle-associated membrane protein (synaptobrevin 2)
1440	13826	AI229304	h,l,hh,jj,kk		ESTs
1441	13831	AI229354	h,l		ESTs
1442	23435	AI229502	n,o		ESTs
1443	18643	AI229702	aa,bb		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1444	13977	AI229707	r		Rattus norvegicus mRNA for class I beta-tubulin, complete cds
1445	15212	AI229753	p,q,t,y,z,ee,ff	ADP-ribosylation factor 2	ADP-ribosylation factor 2
1446	24117	AI229785	cc,dd		ESTs, Highly similar to 2202300B keratin:ISOTYPE=K19 [Rattus norvegicus] [R.norvegicus]
1447	2936	AI229843	kk		ESTs
1448	21446	AI229854	hh		ESTs
1449	13886	AI230116	gg		ESTs
1450	23042	AI230130	s,t,ii	ectonucleoside triphosphate diphosphohydrolase 2	ectonucleoside triphosphate diphosphohydrolase 2
1451	7650	AI230142	w,x		ESTs, Weakly similar to KUCR_RAT Kupffer cell receptor [R.norvegicus]
1452	13887	AI230156	b		ESTs
1453	18528	AI230284	c		ESTs
1454	2372	AI230373	j,k		ESTs
1455	6217	AI230381	p,q		ESTs
1456	23937	AI230430	ii		ESTs
1457	6560	AI230440	t		ESTs
1458	14257	AI230460	c	MARCKS-like protein	MARCKS-like protein
1459	19944	AI230479	b		ESTs
1460	23998	AI230578	s,t,ii		ESTs
1461	22484	AI230591	ll		ESTs, Weakly similar to TES1_RAT TESTIN 1/2 PRECURSOR (CMB-22/CMB-23) [R.norvegicus]
1462	9412	AI230691	f,g		ESTs, Moderately similar to RL34_RAT 60S RIBOSOMAL PROTEIN L34 [R.norvegicus]
1463	18529	AI230716	a,ll		ESTs
1464	23013	AI230743	hh	actin-related protein 3	actin-related protein 3
1465	9171	AI230747	b		ESTs
1466	22387	AI230753	f,g		ESTs, Highly similar to BI3_MOUSE Brain protein I3 [M.musculus]
1467	24270	AI230758	n,o		ESTs, Moderately similar to cargo selection protein (mannose 6 phosphate receptor binding pr; cargo selection protein (mannose 6 phosphate receptor binding protein) [Homo sapiens] [H.sapiens]
1468	14430	AI230798	r	HHs:cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	ESTs, Moderately similar to cyclin-dependent kinase inhibitor 3; CDK2-associated dual specificity phosphatase; cyclin-dependent kinase interacting protein 2; kinase-associated phosphatase; cyclin-dependent kinase interactor 1 [Homo sapiens] [H.sapiens]
1469	13915	AI230826	n,o		ESTs
1470	7520	AI230830	ii		ESTs
1471	8036	AI230884	r		ESTs, Highly similar to HMBA-inducible [Homo sapiens] [H.sapiens]
1472	23730	AI230915	gg		ESTs
1473	13928	AI230939	aa,bb		ESTs
1474	11893	AI230951	w,x		ESTs
1475	16087	AI231011	cc,dd		ESTs
1476	19082	AI231038	s,t		ESTs
1477	13934	AI231044	w,x		ESTs
1478	17903	AI231083	t		ESTs
1479	24072	AI231093	g		ESTs
1480	20845	AI231140	w,x		ESTs, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat [R.norvegicus]
1481	21816	AI231217	ll		ESTs, Highly similar to S611_HUMAN Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha-1) [R.norvegicus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1482	24327	AI231292	gg	Cystatin C (cysteine proteinase inhibitor)	Cystatin C (cysteine proteinase inhibitor)
1483	23304	AI231310	ee,ff	prolyl 4-hydroxylase alpha subunit	prolyl 4-hydroxylase alpha subunit
1484	13966	AI231421	d,t		ESTs
1485	15572	AI231472	f,g	procollagen, type I, alpha 1	procollagen, type I, alpha 1
1486	8004	AI231532	r		ESTs, Highly similar to Z183_HUMAN Zinc finger protein 183 [H.sapiens]
1487	13092	AI231547	jj,kk		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
1488	19271	AI231566	s,t		ESTs, Highly similar to MAX_RAT MAX protein [R.norvegicus]
1489	2422	AI231615	r		ESTs
1490	23012	AI231724	c		ESTs
1491	18402	AI231778	ii		ESTs
1492	6412	AI231787	a		ESTs
1493	15171	AI231792	ee,ff		ESTs, Highly similar to BAG3_MOUSE BAG-family molecular chaperone regulator-3 (BCL-2 binding athanogene-3) (BAG-3) (Bcl-2-binding protein Bis) [M.musculus]
1494	2339	AI231798	hh		ESTs, Highly similar to T-complex expressed gene 2 [Mus musculus] [M.musculus]
1495	23165	AI231799	y,z		ESTs, Moderately similar to i68673 gene X123 protein - human (fragment) [H.sapiens]
1496	7036	AI231801	n,o,cc,dd		ESTs, Weakly similar to A55190 transitional endoplasmic reticulum ATPase (EC 3.6.1.-) [validated] - rat [R.norvegicus]
1497	12435	AI231810	j,k,jj,kk,ll		ESTs
1498	13116	AI231812	c		ESTs, Weakly similar to Y55B1AL.2.p [Caenorhabditis elegans] [C.elegans]
1499	21189	AI231822	h,l		ESTs, Highly similar to mitochondrial carrier homolog 1; mitochondrial carrier homolog 1 isoform b [Mus musculus] [M.musculus]
1500	22591	AI231827	a		ESTs
1501	15173	AI231846	d		ESTs
1502	14013	AI231992	hh		EST
1503	3434	AI232014	y,z,ee,ff		ESTs
1504	19094	AI232021	g		ESTs, Highly similar to SUI1_MOUSE Protein translation factor SUI1 homolog [M.musculus]
1505	8959	AI232128	cc,dd		ESTs
1506	14028	AI232184	d,gg		ESTs
1507	409	AI232268	r	low density lipoprotein receptor-related protein associated protein 1	low density lipoprotein receptor-related protein associated protein 1
1508	2085	AI232270	hh		ESTs, Weakly similar to JC4914 anti-sigma cross-reacting protein homolog I beta precursor - human [H.sapiens]
1509	14031	AI232295	e		ESTs, Moderately similar to B53434 cell surface glycoprotein gp49B form 2 precursor - mouse [M.musculus]
1510	4716	AI232313	c,r	purinergic receptor P2X, ligand-gated ion channel 4	purinergic receptor P2X, ligand-gated ion channel 4
1511	14034	AI232321	n,o		ESTs, Highly similar to CGI-150 protein [Homo sapiens] [H.sapiens]
1512	11873	AI232326	j,k,p,q,y,z		ESTs
1513	15246	AI232332	cc,dd		ESTs
1514	6509	AI232361	ll		ESTs
1515	4891	AI232402	hh		ESTs
1516	3143	AI232408	ll		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1517	11157	AI232494	w,x		ESTs
					ESTs, Weakly similar to S24C_HUMAN Protein transport protein Sec24C (SEC24-related protein C) [H.sapiens]
1518	13645	AI232694	hh		ESTs, Weakly similar to E.coli YCAC like [Caenorhabditis elegans] [C.elegans]
1519	7285	AI232731	gg		ESTs, Highly similar to CG51_HUMAN Protein CGI-51 [H.sapiens]
1520	3100	AI232741	hh		ESTs, Weakly similar to T27038 hypothetical protein Y49E10.2 - Caenorhabditis elegans [C.elegans]
1521	7147	AI232948	hh		ESTs
1522	14088	AI232982	ee,ff		ESTs
1523	4855	AI233024	jj,kk		ESTs
1524	3823	AI233147	y,z		ESTs, Weakly similar to HE47_RAT Probable ATP-dependent RNA helicase p47 [R.norvegicus]
1525	11561	AI233182	b		ESTs
1526	21948	AI233191	hh		ESTs, Weakly similar to YQO9_CAEEL Hypothetical 141.2 kDa protein EEED8.9 in chromosome II [C.elegans]
1527	15107	AI233220	h,l		ESTs, Highly similar to RS18_HUMAN 40S ribosomal protein S18 (KE-3) (KE3) [R.norvegicus]
1528	5228	AI233311	h,l,n,o		ESTs, Highly similar to cytokine receptor-like factor 1; cytokine receptor like molecule 3 [Mus musculus] [M.musculus]
1529	23296	AI233316	hh		ESTs, Weakly similar to ribosomal protein S23 [Rattus norvegicus] [R.norvegicus]
1530	4475	AI233374	n,o		ESTs
1531	14095	AI233468	jj,kk		ESTs
1532	4670	AI233714	w,x		ESTs
1533	14871	AI233743	hh		ESTs
1534	2822	AI233763	hh		ESTs
1535	15085	AI233829	cc,dd,hh	P11 protein	P11 protein
1536	15685	AI233870	hh		ESTs, Weakly similar to PAB1_MOUSE Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) (PABP1) [M.musculus]
1537	2146	AI233965	r		ESTs
1538	3213	AI234095	hh		ESTs
1539	6532	AI234105	j,k,p,q		ESTs
1540	14494	AI234222	a,ee,ff,jj,kk		ESTs
1541	12583	AI234251	hh		ESTs
1542	2765	AI234283	n,o,hh		ESTs
1543	14202	AI234326	cc,dd		EST
1544	17664	AI234496	ii		ESTs
1545	6387	AI234664	cc,dd		ESTs
1546	23964	AI234748	a,kk		ESTs
1547	22152	AI234822	j,k	DEXRAS1 (Dexas1)	DEXRAS1 (Dexas1)
1548	14700	AI234852	jj,kk		ESTs
1549	18444	AI234915	ii	growth and transformation-dependent protein	growth and transformation-dependent protein
1550	13293	AI235032	hh		ESTs, Weakly similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus]
1551	14718	AI235210	d		ESTs
1552	11246	AI235222	jj,kk		ESTs
1553	15004	AI235224	a,l,n,o,x,z,kk	tissue inhibitor of metalloproteinase 1	tissue inhibitor of metalloproteinase 1
1554	6632	AI235277	a,y,z		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1555	11644	AI235282	n,o	HMm:low density lipoprotein receptor-related protein 1	ESTs, Highly similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus]
1556	14722	AI235284	gg		ESTs, Weakly similar to MIC2_HUMAN T-cell surface glycoprotein E2 precursor (E2 antigen) (CD99) (MIC2 protein) (12E7) [H.sapiens]
1557	896	AI235313	h,l		ESTs
1558	14094	AI235377	y,z		ESTs, Moderately similar to synaptic nuclei expressed gene 2 [Homo sapiens] [H.sapiens]
1559	8440	AI235611	b	ZAP 36/annexin IV	ZAP 36/annexin IV
1560	3650	AI235738	r		ESTs, Weakly similar to T42751 sulfonylurea receptor 2 - rat [R.norvegicus]
1561	14642	AI235874	h,l		ESTs, Weakly similar to MCP1_MOUSE Microfibril-associated glycoprotein precursor (MAGP) (MAGP-1) [M.musculus]
1562	2687	AI235877	s,t		ESTs, Highly similar to 2019405A upstream regulator element-binding protein [Rattus norvegicus] [R.norvegicus]
1563	4770	AI235915	d,ll		ESTs
1564	22717	AI235948	g		ESTs, Highly similar to NIDO_RAT NIDOGEN (ENTACTIN) [R.norvegicus]
1565	14776	AI235950	w,x,jj,kk		ESTs
1566	14861	AI236045	c		ESTs
1567	14869	AI236089	aa,bb		ESTs, Weakly similar to T13380 ribokinase homolog - fruit fly (Drosophila melanogaster) [D.melanogaster]
1568	23230	AI236146	t		ESTs
1569	14594	AI236152	b,d,u,v		ESTs
1570	18513	AI236175	c		ESTs, Moderately similar to I54411 MHC RT1-B A-alpha chain - rat (fragment) [R.norvegicus]
1571	14884	AI236212	ll		ESTs
1572	5007	AI236229	s,t,aa,bb		ESTs
1573	22212	AI236294	kk		ESTs, Highly similar to IF6_MOUSE Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) (CAB) (p27(BBP)) [M.musculus]
1574	18610	AI236307	l,m		ESTs
1575	15051	AI236332	j,k,p,q,y,z,ee,ff		ESTs, Highly similar to S43429 diamine N-acetyltransferase (EC 2.3.1.57) - mouse [M.musculus]
1576	4911	AI236405	cc,dd		ESTs, Highly similar to RIKEN cDNA 1700029H06 [Mus musculus] [M.musculus]
1577	19075	AI236473	p,q		ESTs
1578	14901	AI236481	ii		ESTs
1579	9546	AI236520	n,o		ESTs
1580	17950	AI236590	kk		ESTs
1581	18259	AI236601	p,q,ee,ff		ESTs
1582	11445	AI236613	r		ESTs
1583	22939	AI236669	y,z,jj,kk	HMm:REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	ESTs, Highly similar to DPOZ_MOUSE DNA polymerase zeta catalytic subunit (Seizure related protein 4) [M.musculus]
1584	22443	AI236761	ee,ff		ESTs
1585	11404	AI237002	hh	spermidine synthase	spermidine synthase
1586	12098	AI237075	t		ESTs
1587	18151	AI237212	f,g,hh	HHs:hepatitis B virus x interacting protein	ESTs, Highly similar to hepatitis B virus x-interacting protein; HBx-interacting protein; hepatitis B virus x-interacting protein (9.6kD) [Homo sapiens] [H.sapiens]

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1588	3368	AI237331	c		ESTs, Weakly similar to YCE3_HUMAN Hypothetical protein CGI-143 [H.sapiens]
1589	21653	AI237535	a,j,k,p,q,y,z	LPS-induced TNF-alpha factor	LPS-induced TNF-alpha factor
1590	23288	AI237581	u,v		ESTs
1591	11208	AI237586	kk		ESTs, Moderately similar to JC1241 beta-interferon-induced protein - rat [R.norvegicus]
1592	11375	AI237594	u,v		ESTs, Weakly similar to G01614 zinc finger protein 127 - human [H.sapiens]
1593	18854	AI237636	f,g,i,m		ESTs, Weakly similar to CNE6_MOUSE Copine VI (Neuronal-copine) (N-copine) [M.musculus]
1594	3615	AI237645	t	transferrin receptor	transferrin receptor
1595	8759	AI237646	p,q,ee,ff		ESTs
1596	14720	AI237648	gg		ESTs
1597	14840	AI237698	kk		ESTs
1598	14842	AI237724	u,v		ESTs
1599	9501	AI638949	c,f,g,v		ESTs, Moderately similar to chromosome 20 open reading frame 116 [Homo sapiens] [H.sapiens]
1600	16340	AI638955	hh		ESTs, Highly similar to fox-1 homolog (C. elegans) [Mus musculus] [M.musculus]
1601	25854	AI639001	r		ESTs
1602	17214	AI639008	b,h,l		ESTs
1603	23781	AI639012	a,h,i,l,n,o		ESTs, Weakly similar to hypothetical protein MGC2601 [Homo sapiens] [H.sapiens]
1604	17108	AI639017	ll		ESTs, Weakly similar to T17453 ERG-associated protein ESET - mouse [M.musculus]
1605	4035	AI639023	cc,dd		ESTs
1606	15450	AI639035	cc,dd		ESTs
1607	10071	AI639058	a,q,y,z,ee,ff,ll		ESTs, Highly similar to Nedd4 WW binding# protein 4; Nedd4 WW-binding protein 4 [Mus musculus] [M.musculus]
1608	17383	AI639060	h,i,l,w,x		ESTs
1609	25883	AI639076	j		
1610	16514	AI639093	hh		ESTs
1611	22555	AI639103	n,o		ESTs
1612	12400	AI639107	n,o		ESTs
1613	13882	AI639120	b		ESTs
1614	25895	AI639128	jj,kk		ESTs
1615	25899	AI639136	n,o		
1616	5065	AI639139	ll		ESTs
1617	18482	AI639151	gg		ESTs, Highly similar to pinin [Mus musculus] [M.musculus]
1618	20073	AI639152	b,c,u,v		
1619	15379	AI639162	a,jj,kk,ll		ESTs
1620	25907	AI639167	d		ESTs
1621	5159	AI639185	c,u,v		ESTs
1622	19795	AI639197	u,v		EST
1623	19749	AI639203	s,t		ESTs
1624	25918	AI639204	hh		
1625	20021	AI639214	i,m		EST
1626	20614	AI639246	h,i,l,j,k		ESTs
1627	19962	AI639248	aa		
1628	17083	AI639255	e,gg		ESTs
1629	17215	AI639268	h,i,l,n,o,jj,kk		ESTs, Weakly similar to T17307 hypothetical protein DKFZp566O084.1 - human [H.sapiens]
1630	16016	AI639308	ii		ESTs
1631	20461	AI639350	d,q,y,z,kk		ESTs
1632	25964	AI639352	s,t		
1633	18295	AI639381	ee,ff		ESTs

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1634	19152	AI639387	cc,dd		ESTs, Highly similar to RT06_MOUSE Mitochondrial 28S ribosomal protein S6 (MRP-S6) [M.musculus]
1635	20647	AI639402	ii		ESTs
1636	5014	AI639410	cc,dd		ESTs
1637	10097	AI639425	k,kk		ESTs
1638	25997	AI639452	e		
1639	20032	AI639466	n,o		EST
1640	22763	AI639474	e,gg		ESTs
1641	20082	AI639488	d	HMM:transformed mouse 3T3 cell double minute 2	ESTs, Highly similar to A42772 mdm2 protein - rat (fragments) [R.norvegicus]
1642	5998	AI639501	ll		ESTs
1643	20056	AI639504	w,x,ii		ESTs, Weakly similar to T13607 hypothetical protein 87B1.3 - fruit fly (Drosophila melanogaster) [D.melanogaster]
1644	19864	AI639510	d		ESTs
1645	20083	AI639523	s,t,hh		EST, Weakly similar to SPCA_HUMAN Spectrin alpha chain, erythrocyte (Erythroid alpha-spectrin) [H.sapiens]
1646	23219	AJ000347	n,o	3'(2'),5'-bisphosphate nucleotidase	3'(2'),5'-bisphosphate nucleotidase
1647	25235	AJ001290	b,l,m	solute carrier family 5 (inositol transporters), member 3	
1648	7602	AJ001929	f,aa	reticulocalbin	reticulocalbin
1649	20127	AJ011116	j,k,n,o	Endothelial nitric oxide synthase 3	Endothelial nitric oxide synthase 3
1650	2401	AJ011607	u		ESTs, Highly similar to C46642 DNA primase (EC 2.7.7.-) 54K chain - mouse [M.musculus]
1651	20519	C06598	aa,bb		ESTs, Weakly similar to FK506 binding protein 2 (13 kDa) [Rattus norvegicus] [R.norvegicus]
1652	18686	D00729	g,hh	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	Rat mRNA for delta3, delta2-enoyl-CoA isomerase, dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
1653	5049	D10655	g,w,cc,dd,jj,kk	dihydrolipoamide acetyltransferase	dihydrolipoamide acetyltransferase
1653	5050	D10655	f,g,cc,dd	dihydrolipoamide acetyltransferase	dihydrolipoamide acetyltransferase
1654	19053	D12770	aa,bb	solute carrier family 25 (mitochondrial adenine nucleotide translocator) member 4	solute carrier family 25 (mitochondrial adenine nucleotide translocator) member 4
1655	18018	D12771	f,g	Solute carrier family 25, member 5 (adenine nucleotid translocator 2, fibroblast isoform (ATP-ADP carrier protein))	Solute carrier family 25, member 5 (adenine nucleotid translocator 2, fibroblast isoform (ATP-ADP carrier protein))
1656	25257	D13623	s,t		
1656	15281	D13623	a,d		ESTs
1657	25041	D14014	f	Cyclin D1	Cyclin D1
1658	17264	D25233	d	Retinoblastoma 1 (including osteosarcoma)	Retinoblastoma 1 (including osteosarcoma)
1659	16610	D28557	c,f,u,v	cold shock domain protein A	cold shock domain protein A
1660	25276	D28966	s		
1661	25278	D30734	gg	RAS p21 protein activator 2	
1662	9029	D30804	hh	proteasome (prosome, macropain) subunit, alpha type 7	ESTs, Highly similar to S60038 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha chain RC6-I - rat [R.norvegicus]

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1663	1884	D50695	s,t	proteasome (prosome, macropain) 26S subunit, ATPase, 4	proteasome (prosome, macropain) 26S subunit, ATPase, 4
1664	21147	D63772	j,k,p	Solute carrier family 1 A1 (brain glutamate transporter)	Solute carrier family 1 A1 (brain glutamate transporter)
1665	1356	D83538	u,v	phosphatidylinositol 4-kinase	phosphatidylinositol 4-kinase
1666	25306	D84485	u,v		
1667	22762	D89730	bb		ESTs, Highly similar to JC5621 epidermal growth factor-like protein, T16 precursor - rat [R.norvegicus]
1668	20984	D90109	ll	fatty acid Coenzyme A ligase, long chain 2	fatty acid Coenzyme A ligase, long chain 2
1669	25801	E12286	w,x		
1670	20456	H31144	j,k		ESTs, Moderately similar to 1914275A non-receptor Tyr kinase [Homo sapiens] [H.sapiens]
1671	12360	H31456	cc,dd		ESTs
1672	6499	H31625	d		ESTs
1673	13083	H31665	t		ESTs
1674	19278	H31802	jj,kk		EST, Moderately similar to S12207 hypothetical protein (B2 element) - mouse [M.musculus]
1675	4362	H31842	l,m		ESTs
1676	26039	H31982	b		ESTs
1677	6980	H33001	e,y,z,jj,kk		ESTs
1678	24033	H33101	r		ESTs
1679	16524	H33219	e,hh		ESTs
1680	10185	H33426	a,h,jj,kk,ll		ESTs
1681	4405	H33472	c		EST
1682	4407	H33528	h,i,p,q,y,z		ESTs
1683	4418	H33656	c		ESTs
1684	16714	H33660	d		ESTs
1685	15374	H34186	j,k		ESTs, Highly similar to IF39_HUMAN Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) [H.sapiens]
1686	17159	J00797	w,x,aa,bb,hh,ll	alpha-tubulin	alpha-tubulin
9	16130	J01435	bb	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	unknown Glu-Pro dipeptide repeat protein
9	25319	J01435	bb	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	
9	25050	J01435	bb	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	
10	25051	J01436	bb	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	
1687	16260	J01878	u,v		Rat brain-specific identifier sequence RNA, clone p1b224
1688	17285	J02827	c	Branched chain alpha-ketoacid dehydrogenase subunit E1 alpha	Branched chain alpha-ketoacid dehydrogenase subunit E1 alpha
1689	17136	J04035	f,aa,bb	Tropoelastin	Tropoelastin
1690	20549	K01701	b	Oxytocin/neurophysin	Oxytocin/neurophysin
1691	14968	K02815	c	butyrophilin-like 2 (MHC class II associated)	butyrophilin-like 2 (MHC class II associated)
1692	23486	K02816	cc,dd	pR-ET2 encoded oncodevelopmental protein	pR-ET2 encoded oncodevelopmental protein
1693	381	L00124	b,l,m	Elastase 2, pancreatic	Elastase 2, pancreatic



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1694	17508	L08814	ii	Structure specific recognition protein 1	Structure specific recognition protein 1
1695	25354	L13025	g		
1696	25359	L13202	n,o	forkhead box D3	
1697	25371	L17077	e		
1698	6963	L18889	e	calnexin	
1699	24520	L20869	e		Rattus norvegicus pancreatitis associated protein III (PAPIII) mRNA, complete cds
1700	25816	L23863	n,o	POU domain, class 2, transcription factor 3	POU domain, class 2, transcription factor 3
1701	12058	L25387	w	phosphofructokinase, platelet	ESTs, Highly similar to A53047 6-phosphofructokinase (EC 2.7.1.11) - rat [R.norvegicus]
1701	25377	L25387	hh	phosphofructokinase, platelet	
1702	13682	L38482	e	HHs:cell division cycle 34	ESTs, Moderately similar to I54552 hypothetical serine proteinase - rat [R.norvegicus]
1703	11955	L48209	hh	cytochrome c oxidase, subunit VIIa	cytochrome c oxidase, subunit VIIa
1704	17086	M13011	l,m,ll		
1705	20625	M13100	p		
1705	20628	M13100	hh		
1705	20630	M13100	f,g		
1705	18480	M13100	hh		ESTs
1706	25399	M13101	f		
1707	1466	M14050	e	Heat shock 70kD protein 5	ESTs, Heat shock 70kD protein 5
1708	20714	M14972	s,t	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
1709	19255	M15562	c		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
1709	19256	M15562	c		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
1710	25411	M18529	gg		
1711	16427	M21354	f,g	procollagen, type III, alpha 1	procollagen, type III, alpha 1
1712	15049	M24542	aa,bb	HHs:ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	ESTs, Highly similar to A32296 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) Rieske iron-sulfur protein precursor - rat (fragment) [R.norvegicus]
1713	15571	M27207	g	procollagen, type I, alpha 1	procollagen, type I, alpha 1
1714	25438	M32757	l,m		
1715	15580	M33648	y,z		Rat mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase mRNA, complete cds
1716	17211	M34331	cc,dd		Rattus norvegicus mRNA for ribosomal protein L35
1716	26030	M34331	g		Rattus norvegicus mRNA for ribosomal protein L35
11	25439	M35826	bb	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	
1717	9223	M36151	c		Rat mRNA for MHC class II antigen RT1.B-1 beta-chain, Rattus norvegicus MHC class II antigen RT1.B beta chain mRNA, partial cds
1718	21400	M36410	ee,ff,gg	sepiapterin reductase	sepiapterin reductase
1719	17145	M38566	gg	Serine protease inhibitor	Serine protease inhibitor
1720	1586	M57728	c		Rat general mitochondrial matrix processing protease (MPP) mRNA, 3' end
1721	24844	M58040	u,v	transferrin receptor	transferrin receptor
1722	24662	M59786	l,m,jj,kk	Ca channel, voltage-dependent, L type, alpha 1c subunit	Ca channel, voltage-dependent, L type, alpha 1c subunit

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1723	457	M60666	aa	Tropomyosin 1 (alpha)	Tropomyosin 1 (alpha)
1724	17130	M62992	l,m		
1725	10743	M64780	r,jj,kk	Agrin	Agrin
1725	10744	M64780	f	Agrin	Agrin
1726	5733	M81855	d	ATP-binding cassette, sub-family B (MDR/TAP), member 1 (P-glycoprotein/multidrug resistance 1)	ATP-binding cassette, sub-family B (MDR/TAP), member 1 (P-glycoprotein/multidrug resistance 1)
1727	21882	M83740	l,m	dimerization cofactor of hepatocyte nuclear factor-1-alpha	
1728	3762	M86341	s,t	ADP-ribosylarginine hydrolase	ADP-ribosylarginine hydrolase
1729	13489	M91599	cc,dd	Fibroblast growth factor receptor 4	ESTs, Highly similar to JC1450 fibroblast growth factor receptor 4 - rat [R.norvegicus]
1730	25470	M95791	e,aa,bb		
1731	17991	M96626	cc,dd,gg	ATPase, Ca <sup>++</sup> transporting, plasma membrane 3	ATPase, Ca <sup>++</sup> transporting, plasma membrane 3
1732	23698	NM_012489	i	Rattus norvegicus acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A (Acaa), mRNA. 11/22Length = 1619	Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A 1, peroxisomal
1733	15511	NM_012498	ii	Rattus norvegicus Aldehyde reductase 1 (low Km aldose reductase) (5.8 kb PstI fragment, probably the functional gene) (Aldr1), mRNA. 11/22Length = 1339	Aldehyde reductase 1 (low Km aldose reductase) (5.8 kb PstI fragment, probably the functional gene)
1734	583	NM_012505	h,l	Rattus norvegicus ATPase, Na <sup>+</sup> K <sup>+</sup> transporting, alpha 2 (Atp1a2), mRNA. 11/22Length = 519	ATPase, Na <sup>+</sup> K <sup>+</sup> transporting, alpha 2 polypeptide
1735	1745	NM_012513	p,q,ll	Rattus norvegicus Brain derived neurotrophic factor (Bdnf), mRNA. 4/22Length = 185	Brain derived neurotrophic factor
1736	20518	NM_012518	n,o,r	Rattus norvegicus Calmodulin III (Calm3), mRNA. 11/22Length = 691	Calmodulin III
1737	25365	NM_012519	u,v,ll	Rattus norvegicus Ca <sup>++</sup> /calmodulin-dependent protein kinase 2delta subunit (Camk2d), mRNA. 11/22Length = 5637	Ca <sup>++</sup> /calmodulin-dependent protein kinase II, delta subunit
1737	2735	NM_012519	r	Rattus norvegicus Ca <sup>++</sup> /calmodulin-dependent protein kinase 2delta subunit (Camk2d), mRNA. 11/22Length = 5637	Ca <sup>++</sup> /calmodulin-dependent protein kinase II, delta subunit
1737	2736	NM_012519	j,k	Rattus norvegicus Ca <sup>++</sup> /calmodulin-dependent protein kinase 2delta subunit (Camk2d), mRNA. 11/22Length = 5637	Ca <sup>++</sup> /calmodulin-dependent protein kinase II, delta subunit
1738	15741	NM_012520	ll	Rattus norvegicus Catalase (Cat), mRNA. 11/22Length = 2495	Catalase
1739	4467	NM_012529	f,g	Rattus norvegicus creatine kinase, brain (Ckb), mRNA. 11/22Length = 1146	Creatine kinase, brain

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1739	4468	NM_012529	g	Rattus norvegicus creatine kinase, brain (Ckb), mRNA. 11/22Length = 1146	Creatine kinase, brain
1740	11115	NM_012531	f,g	Rattus norvegicus Catecholamine-O-methyltransferase (Comt),mRNA. 11/2Length = 1531	Catecholamine-O-methyltransferase
1740	11116	NM_012531	f,g	Rattus norvegicus Catecholamine-O-methyltransferase (Comt),mRNA. 11/2Length = 1531	Catecholamine-O-methyltransferase
1741	16520	NM_012532	c	Rattus norvegicus Ceruloplasmin (ferroxidase) (Cp), mRNA. 11/22Length = 37	Ceruloplasmin (ferroxidase)
1742	20357	NM_012534	cc,dd	Rattus norvegicus Crystallin, alpha polypeptide A (Cryaa), mRNA. 3/22Length = 156	Crystallin, alpha polypeptide A
1743	20704	NM_012541	aa,bb	Rattus norvegicus cytochrome P450, 1a2 (Cyp1a2), mRNA.11/22Length = 1542	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
1744	1762	NM_012543	f	Rattus norvegicus D site albumin promoter binding protein (Dbp), mRNA. 11/22Length = 1671	D site albumin promoter binding protein
1744	1763	NM_012543	hh	Rattus norvegicus D site albumin promoter binding protein (Dbp), mRNA. 11/22Length = 1671	D site albumin promoter binding protein
1745	225	NM_012544	aa,bb	Rattus norvegicus angiotensin 1 converting enzyme 1 (Ace), mRNA. 11/22Length = 4142	Angiotensin I-converting enzyme (Dipeptidyl carboxypeptidase 1)
1746	23868	NM_012551	a,h,l,p,q,y,z,ee,ff	Rattus norvegicus Early growth response 1 (Egr1), mRNA. 11/22Length = 3112	Early growth response 1
1746	23869	NM_012551	a,h,l,p,q,y,z	Rattus norvegicus Early growth response 1 (Egr1), mRNA. 11/22Length = 3112	Early growth response 1
1746	23871	NM_012551	p,q,y,z,ii	Rattus norvegicus Early growth response 1 (Egr1), mRNA. 11/22Length = 3112	Early growth response 1
1746	23872	NM_012551	p,q,y,z	Rattus norvegicus Early growth response 1 (Egr1), mRNA. 11/22Length = 3112	Early growth response 1
1747	6477	NM_012559	z	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA. 11/2Length = 1358	Fibrinogen, gamma polypeptide
1747	6478	NM_012559	y,z	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA. 11/2Length = 1358	Fibrinogen, gamma polypeptide
1748	619	NM_012565	l,m,n,o	Rattus norvegicus Glucokinase (Gck), mRNA. 11/22Length = 2326	Glucokinase
1749	482	NM_012567	s,t	Rattus norvegicus Gap junction protein, alpha 1, 43 kD(connexin 43) (Gja1), mRNA. 11/2Length = 2768	Gap junction protein, alpha 1, 43 kD (connexin 43)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1750	16025	NM_012578	p,q	Rattus norvegicus Histone H1-(H1f), mRNA. 11/2Length = 1779	Histone H1-0
1750	16026	NM_012578	p,q,s,t,ee,ff	Rattus norvegicus Histone H1-(H1f), mRNA. 11/2Length = 1779	Histone H1-0
1751	16080	NM_012580	p,q,y,z,kk	Rattus norvegicus Heme oxygenase (Hmox1), mRNA. 1/22Length = 87	Heme oxygenase
1752	1708	NM_012581	ii	Rattus norvegicus Homeo box A2 (Hoxa2), mRNA. 1/22Length = 1576	homeobox A2
1752	1709	NM_012581	l,m	Rattus norvegicus Homeo box A2 (Hoxa2), mRNA. 1/22Length = 1576	homeobox A2
1753	20313	NM_012585	b,u,v	Rattus norvegicus 5-hydroxytryptamine (serotonin) receptor 1A (Htr1a), mRNA. 11/22Length = 1269	5-Hydroxytryptamine (serotonin) receptor 1A
1754	15098	NM_012588	bb	Rattus norvegicus insulin-like growth factor binding protein3 (Igfbp3), mRNA. 11/22Length = 2352	Insulin-like growth factor-binding protein (IGF-BP3)
1755	24716	NM_012589	j,k,p,q	Rattus norvegicus Interleukin 6 (interferon, beta 2) (Il6), mRNA. 11/22Length = 146	Interleukin 6 (interferon, beta 2)
1756	4450	NM_012592	c	Rattus norvegicus Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. 11/22Length = 214	Isovaleryl Coenzyme A dehydrogenase
1757	7125	NM_012595	aa,bb	Rattus norvegicus Lactate dehydrogenase B (Ldhb), mRNA. 11/2Length = 1217	Lactate dehydrogenase B
1758	18386	NM_012598	w,x	Rattus norvegicus Lipoprotein lipase (Lpl), mRNA. 11/22Length = 3617	ESTs, Highly similar to JH0790 lipoprotein lipase (EC 3.1.1.34) precursor - rat [R.norvegicus], Lipoprotein lipase
1758	18387	NM_012598	w,x	Rattus norvegicus Lipoprotein lipase (Lpl), mRNA. 11/22Length = 3617	Lipoprotein lipase
1759	2628	NM_012603	a,p,q,y,z	Rattus norvegicus v-myc avian myelocytomatosis viral oncogene homolog (Myc), mRNA. 11/22Length = 2168	Avian myelocytomatosis viral (v-myc) oncogene homolog
1759	2629	NM_012603	a,j,k,p,q,y,z,ee,ff,kk	Rattus norvegicus v-myc avian myelocytomatosis viral oncogene homolog (Myc), mRNA. 11/22Length = 2168	Avian myelocytomatosis viral (v-myc) oncogene homolog
1760	25450	NM_012609	n,o	Rattus norvegicus Neurofibromatosis type 1 (Nf1), mRNA. 11/2Length = 9132	
1761	1298	NM_012610	d	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr),mRNA. 11/2Length = 3259	Nerve growth factor receptor, fast
1761	1299	NM_012610	cc,dd	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr),mRNA. 11/2Length = 3259	Nerve growth factor receptor, fast

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1762	638	NM_012613	aa,bb	Rattus norvegicus natriuretic peptide receptor 1 (Npr1), mRNA. 11/22Length = 468	Natriuretic peptide receptor A/Guanylate cyclase A
1763	24506	NM_012614	c	Rattus norvegicus Neuropeptide Y (Npy), mRNA. 11/22Length = 539	Neuropeptide Y
1764	20589	NM_012618	h,i,n,o,w,x	Rattus norvegicus S1 calcium-binding protein A4 (S1a4), mRNA. 11/22Length = 487	S100 calcium-binding protein A4
1765	15540	NM_012620	a,kk	Rattus norvegicus serine (or cysteine) proteinase inhibitor, member 1 (Pai1), mRNA. 11/22Length = 353	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
1766	25133	NM_012628	gg	Rattus norvegicus Protein kinase C, type I (gamma type) (Prkcg), mRNA. 11/2Length = 3113	
1767	1841	NM_012637	d,jj,kk	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 1 (Ptpn1), mRNA. 1/22Length = 4127	protein tyrosine phosphatase, non-receptor type 1
1767	1844	NM_012637	p,q,y,z	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 1 (Ptpn1), mRNA. 1/22Length = 4127	ESTs, protein tyrosine phosphatase, non-receptor type 1
1768	14924	NM_012645	cc,dd	Rattus norvegicus RT1 class Ib gene (RT1Aw2), mRNA. 11/22Length = 154	ESTs, Weakly similar to A60716 somatotropin Intron-related protein RDE.25 - rat (fragment) [R.norvegicus], RT1 class Ib gene
1769	9423	NM_012649	j,k,y,z	Rattus norvegicus syndecan 4 (Sdc4), mRNA. 11/22Length = 2462	Ryudocan/syndecan 4
1770	16217	NM_012656	c,aa,bb	Rattus norvegicus Secreted acidic cystein-rich glycoprotein (osteonectin) (Sparc), mRNA. 11/2Length = 225	Secreted acidic cystein-rich glycoprotein (osteonectin)
1770	16218	NM_012656	n,o	Rattus norvegicus Secreted acidic cystein-rich glycoprotein (osteonectin) (Sparc), mRNA. 11/2Length = 225	Secreted acidic cystein-rich glycoprotein (osteonectin)
1770	16219	NM_012656	r,gg	Rattus norvegicus Secreted acidic cystein-rich glycoprotein (osteonectin) (Sparc), mRNA. 11/2Length = 225	Secreted acidic cystein-rich glycoprotein (osteonectin)
1770	16220	NM_012656	h,i,aa,bb	Rattus norvegicus Secreted acidic cystein-rich glycoprotein (osteonectin) (Sparc), mRNA. 11/2Length = 225	Secreted acidic cystein-rich glycoprotein (osteonectin)
1770	16221	NM_012656	d	Rattus norvegicus Secreted acidic cystein-rich glycoprotein (osteonectin) (Sparc), mRNA. 11/2Length = 225	Secreted acidic cystein-rich glycoprotein (osteonectin)
1771	21087	NM_012661	cc,dd	Rattus norvegicus steroid sulfatase (Sts), mRNA. 11/22Length = 2472	Steroid sulfatase
1772	16197	NM_012663	j,k	Rattus norvegicus vesicle-associated membrane protein 2 (Vamp2), mRNA. 1/22Length = 271	Vesicle-associated membrane protein (synaptobrevin 2)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1773	24854	NM_012676	aa,bb	Rattus norvegicus troponin T2 (Tnnt2), mRNA. 11/22Length = 196	Troponin T, cardiac
1774	1514	NM_012678	bb	Rattus norvegicus Tropomyosin 4 (Tpm4), mRNA. 11/22Length = 9	Tropomyosin 4
1775	425	NM_012698	hh	Rattus norvegicus Dystrophin (Dmd), mRNA. 11/22Length = 124	Dystrophin
1776	501	NM_012704	ii	Rattus norvegicus prostaglandin E receptor 3 (subtype EP3)(Pter3), mRNA. 1/22Length = 1253	Rat kidney prostaglandin EP3 receptor
1776	503	NM_012704	n,o	Rattus norvegicus prostaglandin E receptor 3 (subtype EP3)(Pter3), mRNA. 1/22Length = 1253	Rat kidney prostaglandin EP3 receptor
1777	4003	NM_012708	e	Rattus norvegicus proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2) (Psm9), mRNA. 11/22Length = 88	Low molecular mass polypeptide 2
1778	322	NM_012715	d,gg	Rattus norvegicus adrenomedullin (Adm), mRNA. 11/22Length = 1395	Adrenomedullin
1779	20888	NM_012716	c,e	Rattus norvegicus Solute carrier 16 (monocarboxylic acid transporter), member 1 (Slc16a1), mRNA. 11/2Length = 332	Solute carrier 16 (monocarboxylic acid transporter), member 1
1779	20889	NM_012716	e,aa,bb	Rattus norvegicus Solute carrier 16 (monocarboxylic acid transporter), member 1 (Slc16a1), mRNA. 11/2Length = 332	Solute carrier 16 (monocarboxylic acid transporter), member 1
1780	1632	NM_012717	u,v	Rattus norvegicus Calcitonin receptor-like receptor (Calcrl),mRNA. 11/22Length = 295	Calcitonin receptor-like receptor
1781	25563	NM_012732	f,g	Rattus norvegicus lipase A, lysosomal acid (Lipa), mRNA.1/22Length = 3144	Cholesterol esterase (pancreatic)
1781	16613	NM_012732	g	Rattus norvegicus lipase A, lysosomal acid (Lipa), mRNA.1/22Length = 3144	Cholesterol esterase (pancreatic)
1782	23806	NM_012733	j,k	Rattus norvegicus retinol-binding protein 1 (Rbp1), mRNA.11/22Length = 695	Retinol-binding protein 1
1783	25264	NM_012735	y,z,gg	Rattus norvegicus Hexokinase 2 (Hk2), mRNA. 11/22Length = 3635	
1784	25650	NM_012736	d	Rattus norvegicus Glycerol-3-phosphate dehydrogenase 2(mitochondrial) (Gpd2), mRNA. 11/2Length = 24	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
1785	1478	NM_012744	n,o	Rattus norvegicus Pyruvate carboxylase (Pc), mRNA. 11/2Length = 3945	Pyruvate carboxylase

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1786	343	NM_012747	n,o	Rattus norvegicus signal transducer and activator of transcription 3 (Stat3), mRNA. 11/22Length = 2924	Signal transducer and activator of transcription 3
1787	8829	NM_012749	j,k,hh,kk	Rattus norvegicus Nucleolin (Ncl), mRNA. 11/22Length = 2142	Nucleolin
1788	3600	NM_012751	a	Rattus norvegicus Glucose transporter 4, insuline-responsive (Glut4), mRNA. 11/22Length = 256	solute carrier family 2 (facilitated glucose transporter), member 4
1788	3601	NM_012751	t	Rattus norvegicus Glucose transporter 4, insuline-responsive (Glut4), mRNA. 11/22Length = 256	solute carrier family 2 (facilitated glucose transporter), member 4
1789	13731	NM_012755	r	Rattus norvegicus Fyn proto-oncogene (Fyn), mRNA. 9/22Length = 1844	Fyn proto-oncogene
1790	15174	NM_012756	m	Rattus norvegicus insulin-like growth factor 2 receptor (Igf2r), mRNA. 11/22Length = 881	Insulin-like growth factor 2 receptor
1791	18066	NM_012762	aa,bb	Rattus norvegicus caspase 1 (Casp1), mRNA. 11/22Length = 129	Interleukin 1beta converting enzyme
1791	18068	NM_012762	e	Rattus norvegicus caspase 1 (Casp1), mRNA. 11/22Length = 129	Interleukin 1beta converting enzyme
1792	17257	NM_012766	e,aa,bb,ee,ff	Rattus norvegicus Cyclin D3 (Cnd3), mRNA. 11/22Length = 1843	Cyclin D3
1792	17261	NM_012766	l,m	Rattus norvegicus Cyclin D3 (Cnd3), mRNA. 11/22Length = 1843	Cyclin D3
1793	5758	NM_012778	p,q,s,t	Rattus norvegicus aquaporin 1 (Aqp1), mRNA. 11/22Length = 2623	Aquaporin 1 (aquaporin channel forming integral protein 28 (CHIP))
1794	104	NM_012779	ii	Rattus norvegicus aquaporin 5 (Aqp5), mRNA. 11/22Length = 1426	Aquaporin 5
1795	449	NM_012786	hh	Rattus norvegicus Cytochrome c oxidase subunit VIII-H (heart/muscle) (Cox8h), mRNA. 11/22Length = 33	Cytochrome c oxidase subunit VIII-H (heart/muscle)
1795	450	NM_012786	f,hh	Rattus norvegicus Cytochrome c oxidase subunit VIII-H (heart/muscle) (Cox8h), mRNA. 11/22Length = 33	Cytochrome c oxidase subunit VIII-H (heart/muscle)
1796	1952	NM_012788	gg	Rattus norvegicus Drosophila discs-large tumor suppressorhomologue (synapse associated protein) (Dlg1), mRNA. 11/22Length = 3256	Drosophila discs-large tumor suppressor homologue (synapse associated protein)
1797	24113	NM_012791	e	Rattus norvegicus Dual Specificity Yak1-related kinase (Dyrk),mRNA. 11/22Length = 284	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1797	18135	NM_012791	e,gg,li	Rattus norvegicus Dual Specificity Yak1-related kinase (Dyrk), mRNA. 11/22Length = 284	ESTs, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a
1798	16947	NM_012793	b,u,v,jj,kk	Rattus norvegicus Guanidinoacetate methyltransferase (Gamt), mRNA. 11/22Length = 924	Guanidinoacetate methyltransferase
1799	961	NM_012796	g	Rattus norvegicus glutathione S-transferase, theta 2 (Gstt2), mRNA. 9/22Length = 1258	glutathione S-transferase, theta 2
1800	10248	NM_012797	b,j,k,s,t,u,jj,kk	Rattus norvegicus Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation) (Id1), mRNA. 1/22Length = 1124	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)
1801	20246	NM_012807	l,m,s	Rattus norvegicus Smoothened (Smoh), mRNA. 1/22Length = 2382	Smoothened
1802	15032	NM_012816	j,k,jj,kk	Rattus norvegicus alpha-methylacyl-CoA racemase (Amacr), mRNA. 11/22Length = 154	alpha-methylacyl-CoA racemase
1803	21350	NM_012823	ii	Rattus norvegicus Annexin III (Lipocortin III) (Anx3), mRNA. 11/22Length = 1454	Annexin A3
1804	2853	NM_012838	n,o	Rattus norvegicus Cystatin beta (Cstb), mRNA. 11/2Length = 59	Cystatin beta
1805	338	NM_012843	r	Rattus norvegicus Epithelial membrane protein 1 (Emp1), mRNA. 11/22Length = 981	Epithelial membrane protein 1
1806	17541	NM_012844	c,d	Rattus norvegicus Epoxide hydrolase 1 (microsomal xenobiotic hydrolase) (Ephx1), mRNA. 1/22Length = 1242	Epoxide hydrolase 1 (microsomal xenobiotic hydrolase)
1807	1249	NM_012850	u,v	Rattus norvegicus Growth hormone - releasing receptor (Ghrhr), mRNA. 11/2Length = 1629	Growth hormone - releasing receptor
1808	18770	NM_012857	hh	Rattus norvegicus Lysosomal associated membrane protein 1 (12 kDa) (Lamp1), mRNA. 11/2Length = 26	Lysosomal associated membrane protein 1 (120 kDa)
1809	13151	NM_012862	n,o,li	Rattus norvegicus Matrix Gla protein (Mgp), mRNA. 11/22Length = 521	Matrix Gla protein
1810	4338	NM_012866	u,v	Rattus norvegicus nuclear transcription factor-Y gamma (Nfyc), mRNA. 11/22Length = 123	CCAAT binding factor of CBF-C/NFY-C
1811	24617	NM_012870	ii	Rattus norvegicus Osteoprotegerin (Opg), mRNA. 11/22Length = 2432	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)
1812	20945	NM_012875	cc,dd	Rattus norvegicus Ribosomal protein L39 (Rpl39), mRNA. 11/22Length = 324	Ribosomal protein L39



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1813	17305	NM_012876	g,hh	Rattus norvegicus Ribosomal protein S29 (Rps29), mRNA. 11/22Length = 318	Ribosomal protein S29
1813	17306	NM_012876	f	Rattus norvegicus Ribosomal protein S29 (Rps29), mRNA. 11/22Length = 318	Ribosomal protein S29
1814	23651	NM_012881	h,l,n,o,w,x	Rattus norvegicus secreted phosphoprotein 1 (Spp1), mRNA. 11/22Length = 1457	Sialoprotein (osteopontin)
1815	16871	NM_012887	y,ll	Rattus norvegicus Thymopoietin (lamina associated polypeptide2) (Tmpt), mRNA. 11/2Length = 358	Thymopoietin (lamina associated polypeptide 2)
1816	16708	NM_012895	u,v	Rattus norvegicus Adenosin kinase (Adk), mRNA. 11/22Length = 1123	Adenosin kinase
1817	187	NM_012903	r	Rattus norvegicus Acid nuclear phosphoprotein 32 (leucine rich) (Anp32), mRNA. 11/2Length = 117	Acid nuclear phosphoprotein 32 (leucine rich)
1818	7196	NM_012904	a,ll	Rattus norvegicus Annexin 1 (p35) (Lipocortin 1) (Anx1), mRNA. 11/22Length = 142	Annexin 1 (p35) (Lipocortin 1)
1819	1834	NM_012905	d	Rattus norvegicus Aortic preferentially expressed gene 1 (Apeg1), mRNA. 11/22Length = 138	Aortic preferentially expressed gene 1
1820	16581	NM_012911	gg	Rattus norvegicus Arrestin, beta 2 (Arrb2), mRNA. 11/22Length = 1758	Arrestin, beta 2
1821	24431	NM_012912	a,p,q,y,z,ee,ff	Rattus norvegicus Activating transcription factor 3 (Atf3), mRNA. 11/22Length = 1893	Activating transcription factor 3
1822	24783	NM_012914	kk	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA. 11/22Length = 4472	ATPase, Ca++ transporting, ubiquitous
1823	6108	NM_012915	c	Rattus norvegicus ATPase inhibitor (rat mitochondrial IF1 protein) (Atp1), mRNA. 11/2Length = 833	ATPase inhibitor (rat mitochondrial IF1 protein)
1824	1765	NM_012919	u,v	Rattus norvegicus Calcium channel subunit alpha 2 delta (dihydropyridine - sensitive L-type) (Cacna2d1), mRNA. 11/22Length = 384	calcium channel, voltage-dependent, alpha2/delta subunit 1
1825	20757	NM_012923	cc,dd	Rattus norvegicus Cyclin G1 (Cng1), mRNA. 11/22Length = 3169	Cyclin G1
1826	1625	NM_012924	gg	Rattus norvegicus Cell surface glycoprotein CD44 (hyaluronate binding protein) (Cd44), mRNA. 4/22Length = 438	Cell surface glycoprotein CD44 (hyaluronate binding protein)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1827	1977	NM_012930	a,w,x,cc,dd	Rattus norvegicus Carnitine palmitoyltransferase 2 (Cpt2), mRNA. 11/22Length = 2296	Carnitine palmitoyltransferase 2
1828	18694	NM_012931	j,k,gg	Rattus norvegicus v-crk-associated tyrosine kinase substrate (Crkas), mRNA. 11/22Length = 3335	v-crk-associated tyrosine kinase substrate
1828	18695	NM_012931	j,k,y,z	Rattus norvegicus v-crk-associated tyrosine kinase substrate (Crkas), mRNA. 11/22Length = 3335	v-crk-associated tyrosine kinase substrate
1829	13723	NM_012935	aa,bb	Rattus norvegicus Crystallin, alpha polypeptide 2 (Cryab), mRNA. 11/21Length = 528	Crystallin, alpha polypeptide 2, ESTs, ESTs, Weakly similar to T46637 transcription factor 1, neural - rat [R.norvegicus]
1830	487	NM_012937	n	Rattus norvegicus crystallin, beta B2 (Crybb2), mRNA. 11/22Length = 735	R.norvegicus CRYBB2 gene (crystallin, beta B2)
1831	190	NM_012940	j,k	Rattus norvegicus Cytochrome P45 1b1 (Cyp1b1), mRNA. 11/2Length = 4964	Cytochrome P450 1b1
1832	20928	NM_012941	l,m	Rattus norvegicus Cytochrom P45 Lanosterol 14 alpha-demethylase (Cyp51), mRNA. 11/22Length = 226	Cytochrom P450 Lanosterol 14 alpha-demethylase
1833	223	NM_012945	a,p,q,ee,ff	Rattus norvegicus Diphtheria toxin receptor (heparin binding epidermal growth factor - like growth factor) (Dtr), mRNA. 11/2Length = 155	Diphtheria toxin receptor (heparin binding epidermal growth factor - like growth factor)
1834	5033	NM_012966	s,t	Rattus norvegicus Heat shock 1 kD protein 1 (chaperonin 1) (Hspe1), mRNA. 11/2Length = 68	Heat shock 10 kD protein 1 (chaperonin 10)
1834	5034	NM_012966	ee,ff	Rattus norvegicus Heat shock 1 kD protein 1 (chaperonin 1) (Hspe1), mRNA. 11/2Length = 68	Heat shock 10 kD protein 1 (chaperonin 10)
1835	2555	NM_012967	a,y,z,kk	Rattus norvegicus Intercellular adhesion molecule 1 (Icam1), mRNA. 11/2Length = 262	Intercellular adhesion molecule 1
1836	22434	NM_012974	l,m	Rattus norvegicus Laminin chain beta 2 (Lamb2), mRNA. 11/2Length = 5581	Laminin chain beta 2
1836	22435	NM_012974	c	Rattus norvegicus Laminin chain beta 2 (Lamb2), mRNA. 11/2Length = 5581	Laminin chain beta 2
1837	956	NM_012976	c,v	Rattus norvegicus Lectin, galactose binding, soluble 5 (Galectin-5) (Lgals5), mRNA. 11/2Length = 872	Lectin, galactose binding, soluble 9 (Galectin-9)
1838	957	NM_012977	ii	Rattus norvegicus Lectin, galactose binding, soluble 9 (Galectin-9) (Lgals9), mRNA. 11/2Length = 1545	Lectin, galactose binding, soluble 9 (Galectin-9)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1838	958	NM_012977	kk	Rattus norvegicus Lectin, galactose binding, soluble 9 (Galectin-9) (Lgals9), mRNA. 11/2Length = 1545	Lectin, galactose binding, soluble 9 (Galectin-9)
1839	571	NM_012982	cc,dd	Rattus norvegicus Msh (Drosophila) homeo box homolog (Msx2), mRNA. 11/2Length = 42	Msh (Drosophila) homeo box homolog
1840	764	NM_012988	ee,ff	Rattus norvegicus Nuclear Factor IA (Nfia), mRNA. 11/2Length = 3368	Nuclear Factor IA
1841	17394	NM_012992	hh,kk	Rattus norvegicus Nucleoplasmin-related protein (Nuclearprotein B23 (Npm1), mRNA. 11/2Length = 1232	Nucleoplasmin-related protein (Nuclear protein B23
1842	19393	NM_012998	h,l	Rattus norvegicus Protein disulfide isomerase (Prolyl4-hydroxylase, beta polypeptide) (P4hb), mRNA. 11/2Length = 246	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)
1843	24263	NM_012999	f	Rattus norvegicus Subtilisin - like endoprotease (Pace4), mRNA. 1/21Length = 4153	Subtilisin - like endoprotease
1843	24264	NM_012999	g	Rattus norvegicus Subtilisin - like endoprotease (Pace4), mRNA. 1/21Length = 4153	Subtilisin - like endoprotease
1844	24718	NM_013003	ii	Rattus norvegicus phosphatidylethanolamine N-methyltransferase (Pemt), mRNA. 11/22Length = 893	Phosphatidylethanolamine N-methyltransferase
1845	1467	NM_013010	ii	Rattus norvegicus Protein kinase, AMP-activated, gamma 1non-catalytic subunit (Prkga1), mRNA. 11/22Length = 1328	Protein kinase, AMP-activated, gamma
1846	25279	NM_013011	p,q	Rattus norvegicus Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (Ywhaz), mRNA. 11/22Length = 1687	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
1846	3404	NM_013011	p,q	Rattus norvegicus Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (Ywhaz), mRNA. 11/22Length = 1687	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
1847	23545	NM_013013	l,m	Rattus norvegicus Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator) (Psap), mRNA. 11/2Length = 2175	Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator)
1848	20178	NM_013014	w,x	Rattus norvegicus Persephin (Pspn), mRNA. 11/22Length = 471	Persephin
1849	20229	NM_013018	kk	Rattus norvegicus Ras-related small GTP binding protein 3A (Rab3a), mRNA. 11/2Length = 743	Ras-related small GTP binding protein 3A

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1850	1338	NM_013022	r	Rattus norvegicus RhoA - binding serine/threonine kinase alpha (ROK - alpha) (Rock2), mRNA. 11/2Length = 447	RhoA - binding serine/threonine kinase alpha (ROK - alpha)
1851	17894	NM_013027	gg	Rattus norvegicus Selenoprotein W muscle 1 (Sepw1), mRNA. 7/21Length = 664	Selenoprotein W muscle 1
1852	17174	NM_013030	l,m	Rattus norvegicus Solute carrier family 34 (sodium phosphate), member 1 (Slc34a1), mRNA. 11/22Length = 244	R.norvegicus ASI mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22
1852	18076	NM_013030	cc,dd	Rattus norvegicus Solute carrier family 34 (sodium phosphate), member 1 (Slc34a1), mRNA. 11/22Length = 244	Solute carrier family 17 (sodium/hydrogen exchanger), member 2
1853	733	NM_013040	j,k	Rattus norvegicus ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (Abcc9), mRNA. 4/22Length = 6628	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
1854	17401	NM_013043	a,p,q,z,ee,ff,kk	Rattus norvegicus Transforming growth factor beta stimulated clone 22 (Tgfb1i4), mRNA. 11/2Length = 1666	Transforming growth factor beta stimulated clone 22
1855	11113	NM_013046	l,k,p,q,u,v,gg	Rattus norvegicus Thyrotropin releasing hormone (Trh), mRNA. 11/22Length = 768	Thyrotropin releasing hormone
1855	11114	NM_013046	k,n,o,y,z,kk	Rattus norvegicus Thyrotropin releasing hormone (Trh), mRNA. 11/22Length = 768	Thyrotropin releasing hormone
1856	24874	NM_013057	r	Rattus norvegicus Coagulation factor III (thromboplastin, tissuefactor) (F3), mRNA. 11/2Length = 1683	Coagulation factor III (thromboplastin, tissue factor)
1857	15253	NM_013058	n,o,s,t	Rattus norvegicus Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (Id3), mRNA. 11/22Length = 568	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
1858	14997	NM_013059	e,ee,ff	Rattus norvegicus alkaline phosphatase, tissue-nonspecific(Alpl), mRNA. 11/22Length = 2415	Tissue-nonspecific ALP alkaline phosphatase
1859	21287	NM_013065	l,m	Rattus norvegicus Protein phosphatase 1, catalytic subunit, beta isoform (Ppp1cb), mRNA. 11/22Length = 276	Protein phosphatase 1, catalytic subunit, beta isoform
1860	16924	NM_013069	c,cc,dd	Rattus norvegicus CD74 antigen (invariant polypeptide of majorhistocompatibility class II antigen-associated) (Cd74), mRNA. 11/2Length = 115	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1860	16925	NM_013069	c,n,o	Rattus norvegicus CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated) (Cd74), mRNA. 11/2Length = 115	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated)
1860	16926	NM_013069	c	Rattus norvegicus CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated) (Cd74), mRNA. 11/2Length = 115	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated)
1860	25676	NM_013069	c,m	Rattus norvegicus CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated) (Cd74), mRNA. 11/2Length = 115	
1861	17181	NM_013073	gg	Rattus norvegicus Protein-L-isoaspartate (D-aspartate) O-methyltransferase (Pcmt1), mRNA. 11/2Length = 1658	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
1861	21830	NM_013073	aa,bb	Rattus norvegicus Protein-L-isoaspartate (D-aspartate) O-methyltransferase (Pcmt1), mRNA. 11/2Length = 1658	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
1862	13283	NM_013078	b	Rattus norvegicus Ornithine carbamoyltransferase (Otc), mRNA. 11/2Length = 1519	Ornithine carbamoyltransferase
1863	1529	NM_013082	hh	Rattus norvegicus syndecan 2 (Sdc2), mRNA. 11/2Length = 2153	Ryudocan/syndecan 2
1864	20242	NM_013084	gg	Rattus norvegicus Acyl-Coenzyme A dehydrogenase, short-branched chain (Acadsb), mRNA. 11/2Length = 1322	Acyl-Coenzyme A dehydrogenase, short-branched chain
1865	20878	NM_013085	b	Rattus norvegicus Urinary plasminogen activator, urokinase (Plau), mRNA. 11/2Length = 1454	Urinary plasminogen activator, urokinase
1866	357	NM_013086	a,j,k,p,q,y,z,ee,ff	Rattus norvegicus CAMP responsive element modulator (Crem), mRNA. 11/2Length = 67	CAMP responsive element modulator
1867	8899	NM_013087	d,f	Rattus norvegicus CD81 antigen (target of antiproliferative antibody 1) (Cd81), mRNA. 11/2Length = 133	CD81 antigen (target of antiproliferative antibody 1)
1868	1521	NM_013091	a,s,t,ee,ff,jj,kk	Rattus norvegicus Tumor necrosis factor receptor (Tnfr1), mRNA. 11/2Length = 213	Tumor necrosis factor receptor superfamily, member 1a
1869	1684	NM_013096	b,c,v	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. 11/2Length = 556	Hemoglobin, alpha 1
1869	1685	NM_013096	b,c,v	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. 11/2Length = 556	Hemoglobin, alpha 1

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1869	1688	NM_013096	c	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. 11/2Length = 556	Hemoglobin, alpha 1
1869	1689	NM_013096	b,c,v	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. 11/2Length = 556	Hemoglobin, alpha 1
1869	26150	NM_013096	c,v	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. 11/2Length = 556	
1870	19949	NM_013106	l,m	Rattus norvegicus Guanine nucleotide binding, protein, alpha inhibiting polypeptide 3 (Gnai3), mRNA. 11/2Length = 372	Guanine nucleotide binding, protein, alpha inhibiting polypeptide 3
1871	23709	NM_013113	f,g	Rattus norvegicus ATPase Na+/K+ transporting beta 1 polypeptide (Atp1b1), mRNA. 11/2Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
1871	23710	NM_013113	hh	Rattus norvegicus ATPase Na+/K+ transporting beta 1 polypeptide (Atp1b1), mRNA. 11/2Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
1872	38	NM_013114	aa,bb	Rattus norvegicus Selectin, platelet (Selp), mRNA. 11/2Length = 3185	Selectin, platelet
1873	7854	NM_013115	h,l	Rattus norvegicus Prostaglandin F receptor (Ptgfr), mRNA. 11/2Length = 3	Prostaglandin F receptor
1874	2005	NM_013127	e,bb	Rattus norvegicus CD38 antigen (ADP-ribosyl cyclase / cyclicADP-ribose hydrolase) (Cd38), mRNA. 11/2Length = 2248	CD38 antigen (ADP-ribosyl cyclase / cyclic ADP-ribose hydrolase)
1875	21840	NM_013128	w,ll	Rattus norvegicus Carboxypeptidase E (Cpe), mRNA. 11/2Length = 292	Carboxypeptidase E
1876	16649	NM_013132	c,gg	Rattus norvegicus Annexin V (Anx5), mRNA. 11/2Length = 1417	Annexin V
1877	5837	NM_013143	cc,dd	Rattus norvegicus Meprin 1 alpha (Mep1a), mRNA. 11/2Length = 2928	Meprin 1 alpha
1878	786	NM_013148	n,o	Rattus norvegicus 5-hydroxytryptamine (serotonin) receptor 5A (Htr5a), mRNA. 11/2Length = 1954	5-hydroxytryptamine (serotonin) receptor 5A
1879	46	NM_013151	p,q	Rattus norvegicus Plasminogen activator, tissue (Plat), mRNA. 11/2Length = 2445	Plasminogen activator, tissue
1880	21682	NM_013154	j,k,p,q,y,z,gg,k	Rattus norvegicus CCAAT/enhancerbinding, protein (C/EBP) delta (Cebpd), mRNA. 11/2Length = 12	CCAAT/enhancerbinding, protein (C/EBP) delta
1880	21683	NM_013154	e,j,k,p,q,y,z,kk	Rattus norvegicus CCAAT/enhancerbinding, protein (C/EBP) delta (Cebpd), mRNA. 11/2Length = 12	CCAAT/enhancerbinding, protein (C/EBP) delta

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1881	24867	NM_013155	kk	Rattus norvegicus Very low density lipoprotein receptor (Vldlr), mRNA. 11/22Length = 2952	Very low density lipoprotein receptor
1882	3430	NM_013156	c,l,m,t,kk	Rattus norvegicus Cathepsin L (Ctsl), mRNA. 11/22Length = 1386	Cathepsin L
1882	3431	NM_013156	c,kk	Rattus norvegicus Cathepsin L (Ctsl), mRNA. 11/22Length = 1386	Cathepsin L
1882	25567	NM_013156	j,k,t,kk	Rattus norvegicus Cathepsin L (Ctsl), mRNA. 11/22Length = 1386	
1883	1310	NM_013159	ll	Rattus norvegicus Insulin degrading enzyme (Ide), mRNA. 11/22Length = 4276	Insulin degrading enzyme
1884	3465	NM_013160	h,l	Rattus norvegicus Max interacting protein 1 (Mxi1), mRNA. 11/22Length = 922	ESTs, Moderately similar to MXI1_RAT MAX interacting protein 1 (MXI1 protein) [R.norvegicus]
1885	200	NM_013161	b,l,m	Rattus norvegicus Pancreatic lipase (Pnlip), mRNA. 11/22Length = 1492	Pancreatic lipase
1886	2012	NM_013173	r	Rattus norvegicus solute carrier family 11 member 2 (Slc11a2), mRNA. 1/22Length = 449	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)
1887	21722	NM_013174	jj,kk	Rattus norvegicus transforming growth factor, beta 3 (Tgfb3), mRNA. 11/22Length = 2633	Transforming growth factor, beta 3
1887	21723	NM_013174	p,q	Rattus norvegicus transforming growth factor, beta 3 (Tgfb3), mRNA. 11/22Length = 2633	Transforming growth factor, beta 3
1888	22306	NM_013179	aa,bb	Rattus norvegicus Hypocretin (orexin) neuropeptide precursor(Hcrt), mRNA. 11/2Length = 585	Hypocretin (orexin) neuropeptide precursor
1889	1314	NM_013181	f	Rattus norvegicus Protein kinase, cAMP dependent, regulatory, type 1 (Prkar1a), mRNA. 11/2Length = 1433	Protein kinase, cAMP dependent, regulatory, type 1
1890	1258	NM_013185	hh	Rattus norvegicus Hemopoietic cell tyrosine kinase (Hck), mRNA. 11/2Length = 1911	Hemopoietic cell tyrosine kinase
1891	1714	NM_013187	a,kk	Rattus norvegicus Phospholipase C, gamma 1 (Plcg1), mRNA. 11/22Length = 516	Phospholipase C, gamma 1
1892	1970	NM_013194	gg	Rattus norvegicus Myosin, heavy polypeptide 9, non-muscle(Myh9), mRNA. 11/22Length = 66	Myosin, heavy polypeptide 9, non-muscle
1893	20754	NM_013195	b	Rattus norvegicus Interleukin 2 receptor, beta chain (Il2rb), mRNA. 11/22Length = 2598	Interleukin 2 receptor, beta chain

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1894	16448	NM_013197	b,c,v	Rattus norvegicus Aminolevulinate synthase 2, delta (Alas2), mRNA. 11/2Length = 1899	Aminolevulinate synthase 2, delta
1895	1693	NM_013199	gg	Rattus norvegicus Dynamin 2 (Dnm2), mRNA. 11/2Length = 3463	Dynamin 2
1896	20855	NM_013200	a,w,x,hh	Rattus norvegicus Carnitine palmitoyltransferase 1, muscle (Cpt1b), mRNA. 11/2Length = 2826	Carnitine palmitoyltransferase 1 beta, muscle isoform
1896	20856	NM_013200	a,w,x,aa,hh,ll	Rattus norvegicus Carnitine palmitoyltransferase 1, muscle (Cpt1b), mRNA. 11/2Length = 2826	Carnitine palmitoyltransferase 1 beta, muscle isoform
1897	20864	NM_013215	b,l,m	Rattus norvegicus aflatoxin B1 aldehyde reductase (Afar), mRNA. 11/2Length = 1272	aflatoxin B1 aldehyde reductase
1898	23362	NM_013216	e	Rattus norvegicus Ras homolog enriched in brain (Rheb), mRNA. 11/2Length = 188	Ras homolog enriched in brain
1899	20728	NM_013217	cc,dd,ee,ff	Rattus norvegicus afadin (AF-6), mRNA. 11/2Length = 5957	afadin
1899	20729	NM_013217	jj,kk	Rattus norvegicus afadin (AF-6), mRNA. 11/2Length = 5957	afadin
1899	20731	NM_013217	gg	Rattus norvegicus afadin (AF-6), mRNA. 11/2Length = 5957	afadin
1899	20732	NM_013217	b,u,v	Rattus norvegicus afadin (AF-6), mRNA. 11/2Length = 5957	afadin
1900	18313	NM_013220	a,kk	Rattus norvegicus ankyrin-like repeat protein (Alrp), mRNA. 11/2Length = 1749	cardiac ankyrin repeat protein
1901	1495	NM_013221	y,z,aa,bb	Rattus norvegicus HMG-box containing protein 1 (Hbp1), mRNA. 11/2Length = 2642	HMG-box containing protein 1
1902	1396	NM_013222	d	Rattus norvegicus growth factor, erv1-like (Gfer), mRNA. 11/2Length = 1226	augmenter of liver regeneration
1903	815	NM_013224	g,h,i,w,x	Rattus norvegicus ribosomal protein S26 (Rps26), mRNA. 11/2Length = 435	ribosomal protein S26
1904	18305	NM_013226	f,h,i,w,x	Rattus norvegicus ribosomal protein L32 (Rpl32), mRNA. 11/2Length = 465	
1905	17972	NM_016989	l,m	Rattus norvegicus adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA. 11/2Length = 2681	adenylate cyclase activating polypeptide 1
1906	64	NM_016991	jj,kk	Rattus norvegicus adrenergic, alpha 1B, receptor (Adra1b), mRNA. 11/2Length = 218	Adrenergic, alpha 1B-, receptor
1907	24868	NM_016992	n,o	Rattus norvegicus arginine vasopressin (Avp), mRNA. 11/2Length = 62	Arginine vasopressin (Diabetes insipidus)
1907	24869	NM_016992	n,o	Rattus norvegicus arginine vasopressin (Avp), mRNA. 11/2Length = 62	Arginine vasopressin (Diabetes insipidus)



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1908	24354	NM_016998	c	Rattus norvegicus Carboxypeptidase A1 (pancreatic) (Cpa1), mRNA. 11/22Length = 131	Carboxypeptidase A1 (pancreatic)
1909	20921	NM_016999	s,t	Rattus norvegicus Cytochrome P450, subfamily IVB, polypeptide1 (Cyp4b1), mRNA. 11/22Length = 192	Cytochrome P450, subfamily IVB, polypeptide 1
1910	8417	NM_017008	aa	Rattus norvegicus Glyceraldehyde-3-phosphate dehydrogenase(Gapd), mRNA. 11/22Length = 1233	Glyceraldehyde-3-phosphate dehydrogenase
1911	24676	NM_017010	aa,bb	Rattus norvegicus Glutamate receptor, ionotropic, N-methyl D-aspartate 1 (Grin1), mRNA. 3/21Length = 4213	Glutamate receptor, ionotropic, N-methyl D-aspartate 1
1912	21013	NM_017014	b	Rattus norvegicus Glutathione-S-transferase, mu type 2 (Yb2) (Gstm2), mRNA. 11/22Length = 155	Glutathione-S-transferase, mu type 2 (Yb2)
1913	17815	NM_017015	w,x	Rattus norvegicus Glucuronidase, beta (Gusb), mRNA. 11/22Length = 2472	Glucuronidase, beta
1914	6598	NM_017020	j,k	Rattus norvegicus Interleukin 6 receptor (Il6r), mRNA. 11/22Length = 4614	Interleukin 6 receptor
1915	17807	NM_017025	h,l	Rattus norvegicus Lactate dehydrogenase A (Ldha), mRNA. 11/22Length = 169	Lactate dehydrogenase A
1916	14247	NM_017031	h,l	Rattus norvegicus Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) (Pde4b), mRNA. 4/22Length = 3133	Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
1917	4500	NM_017037	ii	Rattus norvegicus peripheral myelin protein 22 (Pmp22), mRNA. 11/22Length = 1816	Peripheral myelin protein
1918	3203	NM_017039	c	Rattus norvegicus Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (Ppp2ca), mRNA. 11/22Length = 184	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
1919	24597	NM_017040	b,l,m,u,v	Rattus norvegicus Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (Ppp2cb), mRNA. 11/22Length = 1843	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
1920	24697	NM_017048	u,v,ii	Rattus norvegicus Solute carrier family 4, member 2, anionexchange protein 2 (Slc4a2), mRNA. 11/22Length = 457	Solute carrier family 4, member 2, anion exchange protein 2
1921	24695	NM_017049	c	Rattus norvegicus Solute carrier family 4, member 3, anionexchange protein 3 (Slc4a3), mRNA. 11/22Length = 3877	Solute carrier family 4, member 3, anion exchange protein 3

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1922	20875	NM_017050	hh	Rattus norvegicus Superoxide dismutase 1, soluble (Sod1), mRNA.12/21Length = 65	Superoxide dismutase 1, soluble
1922	20876	NM_017050	r	Rattus norvegicus Superoxide dismutase 1, soluble (Sod1), mRNA.12/21Length = 65	Superoxide dismutase 1, soluble
1923	1876	NM_017052	w,x	Rattus norvegicus Sorbitol dehydrogenase (Sord), mRNA. 11/22Length = 1358	Sorbitol dehydrogenase
1924	910	NM_017059	d	Rattus norvegicus bcl2-associated X protein (Bax), mRNA. 11/22Length = 579	Bcl2-associated X protein
1924	911	NM_017059	d	Rattus norvegicus bcl2-associated X protein (Bax), mRNA. 11/22Length = 579	Bcl2-associated X protein
1924	912	NM_017059	d,l,m	Rattus norvegicus bcl2-associated X protein (Bax), mRNA. 11/22Length = 579	Bcl2-associated X protein
1925	19549	NM_017060	h,l	Rattus norvegicus Hras-revertant gene 17 (Hrev17), mRNA. 1/22Length = 966	ESTs
1926	1942	NM_017061	f,li	Rattus norvegicus lysyl oxidase (Lox), mRNA. 11/22Length = 4557	Lysyl oxidase
1926	1943	NM_017061	s,t	Rattus norvegicus lysyl oxidase (Lox), mRNA. 11/22Length = 4557	Lysyl oxidase
1927	1427	NM_017063	hh	Rattus norvegicus Importin beta (Impnb), mRNA. 11/2Length = 2991	Importin beta
1928	6653	NM_017068	d	Rattus norvegicus Lysosomal-associated membrane protein 2 (Lamp2), mRNA. 11/2Length = 1548	Lysosomal-associated membrane protein 2
1928	6654	NM_017068	b,v	Rattus norvegicus Lysosomal-associated membrane protein 2 (Lamp2), mRNA. 11/2Length = 1548	Lysosomal-associated membrane protein 2
1929	11152	NM_017073	c,s,t,kk	Rattus norvegicus Glutamine synthetase (glutamate-ammonialigase) (Glu), mRNA. 11/2Length = 2793	Glutamine synthetase (glutamate-ammonia ligase)
1929	11153	NM_017073	y,kk	Rattus norvegicus Glutamine synthetase (glutamate-ammonialigase) (Glu), mRNA. 11/2Length = 2793	Glutamine synthetase (glutamate-ammonia ligase)
1930	18956	NM_017075	aa	Rattus norvegicus Acetyl-Co A acetyltransferase 1, mitochondrial (Acat1), mRNA. 11/2Length = 1715	Acetyl-Co A acetyltransferase 1, mitochondrial
1930	18957	NM_017075	r,s,t,li	Rattus norvegicus Acetyl-Co A acetyltransferase 1, mitochondrial (Acat1), mRNA. 11/2Length = 1715	Acetyl-Co A acetyltransferase 1, mitochondrial
1931	923	NM_017076	a,p,q,y,z,ee,ff	Rattus norvegicus Tumor-associated glycoprotein pE4 (Tage4), mRNA. 11/2Length = 2171	Tumor-associated glycoprotein pE4

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1932	1523	NM_017079	h,i,n,o,w,x	Rattus norvegicus CD1D antigen (Cd1d), mRNA. 11/2Length = 1835	CD1D antigen
1933	22552	NM_017087	n,o	Rattus norvegicus biglycan (Bgn), mRNA. 11/22Length = 2446	Small proteoglycan I (biglycan), bone (BSPG1) (bone/cartilage proteoglycan 1 precursor)
1934	1383	NM_017088	ii	Rattus norvegicus GDP-dissociation inhibitor 1 (Gdi1), mRNA. 11/2Length = 139	GDP-dissociation inhibitor 1
1935	23665	NM_017092	u,v	Rattus norvegicus Bruton agammaglobulinemia tyrosine kinase (Tyro3), mRNA. 12/2Length = 3726	Bruton agammaglobulinemia tyrosine kinase
1936	10886	NM_017094	ii	Rattus norvegicus growth hormone receptor (Ghr), mRNA. 11/22Length = 295	Growth hormone receptor
1936	10887	NM_017094	jj,kk	Rattus norvegicus growth hormone receptor (Ghr), mRNA. 11/22Length = 295	Growth hormone receptor
1936	10888	NM_017094	e,r,hh	Rattus norvegicus growth hormone receptor (Ghr), mRNA. 11/22Length = 295	Growth hormone receptor
1937	2150	NM_017097	a,ii	Rattus norvegicus Cathepsin C (dipeptidyl peptidase I) (Ctsc), mRNA. 11/2Length = 185	Cathepsin C (dipeptidyl peptidase I)
1938	15517	NM_017099	c	Rattus norvegicus potassium inwardly-rectifying channel, subfamily J, member 8 (Kcnj8), mRNA. 11/22Length = 158	Inwardly rectifying potassium channel gene, subfamily J-8 (ATP sensitive)
1939	4391	NM_017101	s,t	Rattus norvegicus Peptidylprolyl Isomerase A (cyclophilin A)(Ppia), mRNA. 11/22Length = 743	Peptidylprolyl isomerase A (cyclophilin A)
1940	15776	NM_017108	u,v	Rattus norvegicus potassium voltage-gated channel, subfamily H (eag-related), member 3 (Kcnh3), mRNA. 11/22Length = 3715	potassium voltage-gated channel, subfamily H (eag-related), member 3
1941	20745	NM_017113	f,g	Rattus norvegicus granulin (Gm), mRNA. 11/22Length = 2113	granulin
1941	20746	NM_017113	j,cc,dd,gg	Rattus norvegicus granulin (Gm), mRNA. 11/22Length = 2113	granulin
1942	1375	NM_017122	n,o	Rattus norvegicus hippocalcin (Hpca), mRNA. 11/22Length = 1561	hippocalcin
1943	1435	NM_017125	kk	Rattus norvegicus CD63 antigen (Cd63), mRNA. 11/22Length = 86	Cd63 antigen
1944	21662	NM_017126	a,ee,ff	Rattus norvegicus ferredoxin 1 (Fdx1), mRNA. 11/22Length = 838	ferredoxin 1
1944	21663	NM_017126	a,h,l,p,q,y,z,ee,ff	Rattus norvegicus ferredoxin 1 (Fdx1), mRNA. 11/22Length = 838	ferredoxin 1

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1945	24522	NM_017130	u,v	Rattus norvegicus neuraminidase 2 (Neu2), mRNA. 11/22Length = 166	neuraminidase 2
1946	167	NM_017131	b,e,u,v,li	Rattus norvegicus calsequestrin 2 (Casq2), mRNA. 11/22Length = 1681	calsequestrin 2
1947	20916	NM_017132	d	Rattus norvegicus reticulocalbin 2 (Rcn2), mRNA. 11/22Length = 219	reticulocalbin 2
1948	16681	NM_017136	li	Rattus norvegicus squalene epoxidase (Sqle), mRNA. 11/22Length = 2199	squalene epoxidase
1949	24885	NM_017138	h,l,w,x	Rattus norvegicus laminin receptor 1 (67kD, ribosomal protein SA) (Lamr1), mRNA. 11/22Length = 118	laminin receptor 1
1949	24886	NM_017138	h,l,w,x	Rattus norvegicus laminin receptor 1 (67kD, ribosomal protein SA) (Lamr1), mRNA. 11/22Length = 118	laminin receptor 1
1950	492	NM_017140	l,m,n,aa	Rattus norvegicus dopamine receptor D3 (Drd3), mRNA. 11/22Length = 1481	dopamine receptor 3
1951	24106	NM_017141	s,t,bb	Rattus norvegicus DNA polymerase beta (Polb), mRNA. 11/22Length = 3298	DNA polymerase beta
1951	24107	NM_017141	li	Rattus norvegicus DNA polymerase beta (Polb), mRNA. 11/22Length = 3298	DNA polymerase beta
1952	15364	NM_017147	li	Rattus norvegicus cofilin 1 (Cfl1), mRNA. 11/22Length = 139	cofilin 1, non-muscle
1952	15365	NM_017147	aa,bb,li	Rattus norvegicus cofilin 1 (Cfl1), mRNA. 11/22Length = 139	cofilin 1, non-muscle
1953	13392	NM_017148	e	Rattus norvegicus cysteine rich protein 1 (Csrp1), mRNA. 11/22Length = 143	cysteine rich protein 1
1954	17287	NM_017149	li	Rattus norvegicus mesenchyme homeo box 2 (Meox2), mRNA. 11/22Length = 2244	mesenchyme homeobox 2
1955	16953	NM_017151	g	Rattus norvegicus ribosomal protein S15 (Rps15), mRNA. 11/22Length = 487	ribosomal protein S15
1955	16954	NM_017151	gg	Rattus norvegicus ribosomal protein S15 (Rps15), mRNA. 11/22Length = 487	ribosomal protein S15
1955	16955	NM_017151	l,m,s,t	Rattus norvegicus ribosomal protein S15 (Rps15), mRNA. 11/22Length = 487	ribosomal protein S15
1956	21975	NM_017154	d,e,j,k,n,o,y,z, kk	Rattus norvegicus xanthine dehydrogenase (Xdh), mRNA. 11/22Length = 4198	xanthine dehydrogenase
1957	17104	NM_017160	h,l	Rattus norvegicus ribosomal protein S6 (Rps6), mRNA. 11/22Length = 81	ribosomal protein S6

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SEQ.ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1957	17105	NM_017160	h,l	Rattus norvegicus ribosomal protein S6 (Rps6), mRNA. 11/22Length = 81	ribosomal protein S6
1957	17106	NM_017160	n,o	Rattus norvegicus ribosomal protein S6 (Rps6), mRNA. 11/22Length = 81	ribosomal protein S6
1958	17686	NM_017165	hh	Rattus norvegicus glutathione peroxidase 4 (Gpx4), mRNA. 11/22Length = 872	glutathione peroxidase 4
1959	20702	NM_017166	j,k,y,z	Rattus norvegicus stathmin 1 (Stmn1), mRNA. 11/22Length = 154	Leukemia-associated cytosolic phosphoprotein stathmin
1960	20919	NM_017172	a	Rattus norvegicus zinc finger protein 36, C3H type-like 1 (Zfp361), mRNA. 5/22Length = 2741	zinc finger protein 36, C3H type-like 1
1961	17301	NM_017173	c,f,g,j,k,y,z	Rattus norvegicus serine (or cysteine) proteinase inhibitor, clade H, member 1 (Serpinh1), mRNA. 11/22Length = 263	serine proteinase inhibitor, clade H (heat shock protein 47), member 1
1962	9378	NM_017174	jj,kk	Rattus norvegicus phospholipase A2, group 5 (Pla2g5), mRNA. 11/22Length = 183	phospholipase A2, group V
1963	19031	NM_017180	p,q	Rattus norvegicus T-cell death associated gene (Tdag), mRNA. 11/22Length = 1353	T-cell death associated gene
1964	1488	NM_017182	h	Rattus norvegicus H2A histone family, member Y (H2afy), mRNA. 1/22Length = 157	H2A histone family, member Y
1965	5676	NM_017188	ee,ff	Rattus norvegicus UNC-119 homolog (C. elegans) (Unc119), mRNA. 11/22Length = 1264	UNC-119 homolog (C. elegans)
1966	9124	NM_017199	h,l,hh	Rattus norvegicus signal sequence receptor 4 (Ssr4), mRNA. 11/22Length = 757	signal sequence receptor, delta
1967	20779	NM_017201	b,l,m	Rattus norvegicus S-adenosylhomocysteine hydrolase (Ahcy), mRNA. 11/22Length = 229	S-adenosylhomocysteine hydrolase
1968	14694	NM_017202	aa	Rattus norvegicus cytochrome c oxidase, subunit 4a (Cox4a), mRNA. 11/22Length = 696	cytochrome c oxidase, subunit IVa
1969	24859	NM_017206	h,l	Rattus norvegicus solute carrier family 6, member 6 (Sic6a6), mRNA. 11/22Length = 2489	Solute carrier 6 ,member 6 (taurine transporter)
1970	13938	NM_017212	jj,kk	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA. 11/22Length = 524	microtubule-associated protein tau
1970	13940	NM_017212	a	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA. 11/22Length = 524	microtubule-associated protein tau

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1971	1527	NM_017220	ee,ff	Rattus norvegicus 6-pyruvoyl-tetrahydropterin synthase (Pts), mRNA. 11/22Length = 1176	6-pyruvoyl-tetrahydropterin synthase
1971	20632	NM_017220	aa,bb	Rattus norvegicus 6-pyruvoyl-tetrahydropterin synthase (Pts), mRNA. 11/22Length = 1176	ESTs
1971	19928	NM_017220	l,m	Rattus norvegicus 6-pyruvoyl-tetrahydropterin synthase (Pts), mRNA. 11/22Length = 1176	ESTs
1972	11989	NM_017222	hh	Rattus norvegicus solute carrier family 1, member 2 (Slc1a2), mRNA. 11/22Length = 4269	ESTs
1972	18967	NM_017222	r	Rattus norvegicus solute carrier family 1, member 2 (Slc1a2), mRNA. 11/22Length = 4269	ESTs
1973	1510	NM_017224	ll	Rattus norvegicus solute carrier family 22 (organic anion transporter), member 6 (Slc22a6), mRNA. 1/22Length = 2227	solute carrier family 22 (organic anion transporter), member 6
1974	15108	NM_017226	u,v	Rattus norvegicus peptidyl arginine deiminase, type 2 (Pdi2),mRNA. 11/22Length = 457	ESTs, Highly similar to RS18_HUMAN 40S ribosomal protein S18 (KE-3) (KE3) [R.norvegicus], peptidyl arginine deiminase, type II
1974	18148	NM_017226	n,o	Rattus norvegicus peptidyl arginine deiminase, type 2 (Pdi2),mRNA. 11/22Length = 457	peptidyl arginine deiminase, type II
1975	24598	NM_017231	hh	Rattus norvegicus phosphatidylinositol transfer protein (Pitpn), mRNA. 11/22Length = 1638	phosphatidylinositol transfer protein
1976	20193	NM_017232	p,q	Rattus norvegicus prostaglandin-endoperoxide synthase 2 (Pgs2), mRNA. 11/22Length = 444	prostaglandin-endoperoxide synthase 2
1977	15598	NM_017236	ii	Rattus norvegicus phosphatidylethanolamine binding protein (Pbp), mRNA. 11/22Length = 175	phosphatidylethanolamine binding protein
1978	1498	NM_017239	d	Rattus norvegicus myosin heavy chain, polypeptide 6 (Myh6),mRNA. 11/22Length = 593	myosin heavy chain, polypeptide 6, cardiac muscle, alpha
1978	1497	NM_017239	d	Rattus norvegicus myosin heavy chain, polypeptide 6 (Myh6),mRNA. 11/22Length = 593	myosin heavy chain, polypeptide 6, cardiac muscle, alpha
1979	20482	NM_017240	c,g	Rattus norvegicus myosin heavy chain, polypeptide 7 (Myh7),mRNA. 11/22Length = 5925	myosin heavy chain, cardiac muscle, fetal

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1979	20483	NM_017240	d	Rattus norvegicus myosin heavy chain, polypeptide 7 (Myh7), mRNA. 11/22Length = 5925	myosin heavy chain, cardiac muscle, fetal
1979	20484	NM_017240	e	Rattus norvegicus myosin heavy chain, polypeptide 7 (Myh7), mRNA. 11/22Length = 5925	myosin heavy chain, cardiac muscle, fetal
1979	3780	NM_017240	c,g	Rattus norvegicus myosin heavy chain, polypeptide 7 (Myh7), mRNA. 11/22Length = 5925	EST
1980	17561	NM_017245	l,m	Rattus norvegicus eukaryotic translation elongation factor 2(Eef2), mRNA. 11/22Length = 2626	eukaryotic translation elongation factor 2
1980	17563	NM_017245	h,l	Rattus norvegicus eukaryotic translation elongation factor 2(Eef2), mRNA. 11/22Length = 2626	eukaryotic translation elongation factor 2
1981	17501	NM_017248	l,m	Rattus norvegicus heterogeneous nuclear ribonucleoprotein A1(Hnrpa1), mRNA. 11/22Length = 1696	heterogeneous nuclear ribonucleoprotein A1
1981	17502	NM_017248	l,m	Rattus norvegicus heterogeneous nuclear ribonucleoprotein A1(Hnrpa1), mRNA. 11/22Length = 1696	heterogeneous nuclear ribonucleoprotein A1
1982	16601	NM_017252	s,t	Rattus norvegicus POU domain, class 3, transcription factor 4(Pou3f4), mRNA. 11/22Length = 125	POU domain, class 3, transcription factor 4
1983	1496	NM_017255	aa,bb	Rattus norvegicus purinergic receptor P2Y, G-protein coupled 2 (P2ry2), mRNA. 11/22Length = 211	purinergic receptor P2Y, G-protein coupled 2
1984	19	NM_017258	p,q	Rattus norvegicus B-cell translocation gene 1 (Btg1), mRNA. 11/22Length = 1464	B-cell translocation gene 1, anti-proliferative
1985	15300	NM_017259	p,q,kk	Rattus norvegicus B-cell translocation gene 2 (Btg2), mRNA. 11/22Length = 2519	Early induced gene, B-cell translocation gene 2
1985	15301	NM_017259	j,k,p,q,y,z,gg	Rattus norvegicus B-cell translocation gene 2 (Btg2), mRNA. 11/22Length = 2519	Early induced gene, B-cell translocation gene 2
1985	15299	NM_017259	y,z	Rattus norvegicus B-cell translocation gene 2 (Btg2), mRNA. 11/22Length = 2519	Early induced gene, B-cell translocation gene 2
1986	7593	NM_017260	w,x	Rattus norvegicus arachidonate 5-lipoxygenase activating protein (Alox5ap), mRNA. 11/22Length = 54	Arachidonate 5-lipoxygenase activating protein
1986	7594	NM_017260	w,x,li	Rattus norvegicus arachidonate 5-lipoxygenase activating protein (Alox5ap), mRNA. 11/22Length = 54	Arachidonate 5-lipoxygenase activating protein

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1987	20600	NM_017268	ii	Rattus norvegicus 3-hydroxy-3-methylglutaryl-Coenzyme Asynthase 1 (Hmgcs1), mRNA. 11/22Length = 3275	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
1987	20601	NM_017268	r	Rattus norvegicus 3-hydroxy-3-methylglutaryl-Coenzyme Asynthase 1 (Hmgcs1), mRNA. 11/22Length = 3275	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
1988	20913	NM_017272	n,o	Rattus norvegicus aldehyde dehydrogenase family 1, subfamily A4 (Aldh1a4), mRNA. 11/22Length = 224	aldehyde dehydrogenase family 1, subfamily A4
1989	20281	NM_017274	gg	Rattus norvegicus glycerol-3-phosphate acyltransferase, mitochondrial (Gpam), mRNA. 11/22Length = 2646	glycerol-3-phosphate acyltransferase, mitochondrial
1990	17959	NM_017277	s,t	Rattus norvegicus adaptor protein complex AP-1, beta 1 subunit (Ap1b1), mRNA. 11/22Length = 3679	Adaptor protein complex AP-1, beta 1 subunit
1991	15142	NM_017278	l,m	Rattus norvegicus proteasome (prosome, macropain) subunit, alpha type 1 (Psm1), mRNA. 11/22Length = 1174	proteasome (prosome, macropain) subunit, alpha type 1
1992	15538	NM_017283	r	Rattus norvegicus proteasome (prosome, macropain) subunit, alpha type 6 (Psm6), mRNA. 11/22Length = 932	proteasome (prosome, macropain) subunit, alpha type 6
1993	20579	NM_017288	aa,bb	Rattus norvegicus sodium channel, voltage-gated, type 1, beta polypeptide (Scn1b), mRNA. 11/22Length = 149	sodium channel, voltage-gated, type I, beta polypeptide
1994	12347	NM_017290	ll	Rattus norvegicus ATPase, Ca++ transporting, cardiac muscle,slow twitch 2 (Atp2a2), mRNA. 11/22Length = 5648	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
1994	12349	NM_017290	aa	Rattus norvegicus ATPase, Ca++ transporting, cardiac muscle,slow twitch 2 (Atp2a2), mRNA. 11/22Length = 5648	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
1995	82	NM_017297	ii	Rattus norvegicus potassium inwardly-rectifying channel, subfamily J, member 5 (Kcnj5), mRNA. 1/22Length = 3156	potassium inwardly-rectifying channel, subfamily J, member 5
1996	23825	NM_017299	cc,dd	Rattus norvegicus solute carrier family 19, member 1 (Slc19a1), mRNA. 11/22Length = 242	solute carrier family 19 (sodium/hydrogen exchanger), member 1
1997	1028	NM_017304	ii	Rattus norvegicus potassium voltage gated channel, shakerrelated subfamily, beta member 2 (Kcnab2), mRNA. 11/22Length = 17	potassium voltage gated channel, shaker related subfamily, beta member 2
1998	14004	NM_017305	aa,bb	Rattus norvegicus Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (Glcir), mRNA. 11/22Length = 1382	glutamate-cysteine ligase , modifier subunit



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1999	18687	NM_017306	hh	Rattus norvegicus dodecenoyl-coenzyme A delta isomerase (Dci), mRNA. 11/22Length = 987	Rat mRNA for delta3, delta2-enoyl-CoA isomerase, dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
2000	16844	NM_017311	n,o	Rattus norvegicus ATP synthase, H <sup>+</sup> -transporting, mitochondrial F complex, subunit c, isoform 1 (Atp5g1), mRNA. 11/22Length = 561	ATP synthase, H <sup>+</sup> -transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1
2001	1904	NM_017315	u,v	Rattus norvegicus sodium-coupled ascorbic acid transporter 1 (SVCT1), mRNA. 11/2Length = 2472	Rat VL30 element mRNA
2002	1894	NM_017320	b,l,m,kk	Rattus norvegicus cathepsin S (Ctss), mRNA. 8/22Length = 133	cathepsin S
2003	24533	NM_017328	n,o	Rattus norvegicus phosphoglycerate mutase 2 (Pgam2), mRNA. 11/22Length = 798	Phosphoglycerate mutase 2
2004	24248	NM_017332	e,gg	Rattus norvegicus fatty acid synthase (Fasn), mRNA. 11/22Length = 9136	fatty acid synthase
2005	355	NM_017334	a,j,k,p,q,y,z,ee,ff	Rattus norvegicus CAMP responsive element modulator (Crem),mRNA. 1/22Length = 436	CAMP responsive element modulator
2005	356	NM_017334	a,j,k,p,q,kk	Rattus norvegicus CAMP responsive element modulator (Crem),mRNA. 1/22Length = 436	CAMP responsive element modulator
2006	16382	NM_017343	cc,dd	Rattus norvegicus myosin regulatory light chain (MRLCB), mRNA. 6/21Length = 1139	myosin regulatory light chain
2006	20848	NM_017343	bb,hh,jj,kk	Rattus norvegicus myosin regulatory light chain (MRLCB), mRNA. 6/21Length = 1139	Rat mRNA for myosin regulatory light chain (RLC)
2006	20849	NM_017343	gg	Rattus norvegicus myosin regulatory light chain (MRLCB), mRNA. 6/21Length = 1139	Rat mRNA for myosin regulatory light chain (RLC)
2007	17782	NM_017344	e	Rattus norvegicus glycogen synthase kinase 3 alpha (Gsk3a), mRNA. 11/22Length = 2155	glycogen synthase kinase 3 alpha
2008	15037	NM_017347	e,r	Rattus norvegicus mitogen activated protein kinase 3 (Mapk3), mRNA. 11/22Length = 1238	mitogen activated protein kinase 3
2009	468	NM_017348	w,x	Rattus norvegicus choline transporter (CHOT1), mRNA. 11/2Length = 3972	choline transporter
2010	24428	NM_017356	ll	Rattus norvegicus neural visinin-like Ca <sup>2+</sup> -binding protein type3 (NVP-3), mRNA. 11/2Length = 115	neural visinin-like Ca <sup>2+</sup> -binding protein type 3

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2011	17202	NM_017357	gg	Rattus norvegicus neural visinin-like Ca2+-binding protein type2 (NVP-2), mRNA. 11/2Length = 663	neural visinin-like Ca2+-binding protein type 2
2012	20417	NM_017359	h,i,hh	Rattus norvegicus ras-related protein rab1 (Rab1), mRNA. 11/2Length = 991	ras-related protein rab10
2013	20232	NM_017364	u,v	Rattus norvegicus Pancreas zinc finger protein, see also D1Bda102 (Znf146), mRNA. 5/22Length = 1578	Pancreas zinc finger protein, see also D1Bda102
2014	1581	NM_017365	l,p,q,s,t	Rattus norvegicus PDZ and LIM domain 1 (Pdlim1), mRNA. 11/22Length = 1392	PDZ and LIM domain 1 (elfin)
2015	20536	NM_019122	b,l,m,u,v	Rattus norvegicus Synaptotagmin 3 (Syt3), mRNA. 11/22Length = 296	Synaptotagmin 3
2016	20778	NM_019124	ll	Rattus norvegicus rabaptin 5 (LOC5419), mRNA. 11/22Length = 3465	rabaptin 5
2017	20318	NM_019127	n,o	Rattus norvegicus Interferon, beta 1, fibroblast (Ifnb1), mRNA. 11/22Length = 555	Interferon, beta 1, fibroblast
2018	455	NM_019131	b,u,v	Rattus norvegicus tropomyosin 1, alpha (Tpm1), mRNA. 11/22Length = 14	Tropomyosin 1 (alpha)
2018	461	NM_019131	b,l,m	Rattus norvegicus tropomyosin 1, alpha (Tpm1), mRNA. 11/22Length = 14	Tropomyosin 1 (alpha)
2019	15975	NM_019132	ii	Rattus norvegicus Guanine nucleotide-binding protein G-s, alphasubunit, Genbank no U51565 (Gnas), mRNA. 11/22Length = 1738	Guanine nucleotide-binding protein G-s, alpha subunit
2020	16227	NM_019137	l,m	Rattus norvegicus early growth response 4 (Egr4), mRNA. 11/22Length = 2145	Zinc-finger transcription factor NGFI-C (early response gene)
2021	14973	NM_019140	aa	Rattus norvegicus protein tyrosine phosphatase, receptor type, D (Ptprd), mRNA. 11/22Length = 6469	Protein tyrosine phosphatase, receptor type, D
2022	5618	NM_019143	s,t	Rattus norvegicus Fibronectin 1 (Fn1), mRNA. 11/22Length = 8329	Fibronectin 1
2022	5622	NM_019143	n,o	Rattus norvegicus Fibronectin 1 (Fn1), mRNA. 11/22Length = 8329	Fibronectin 1
2023	278	NM_019150	aa,bb	Rattus norvegicus urocortin (Ucn), mRNA. 11/22Length = 579	urocortin
2024	20863	NM_019152	cc,dd	Rattus norvegicus calpain 1 (Capn1), mRNA. 11/22Length = 2917	calpain 1
2025	6451	NM_019153	f,g	Rattus norvegicus fibulin 5 (Fbln5), mRNA. 11/22Length = 234	fibulin 5
2026	24362	NM_019156	jj,kk	Rattus norvegicus vitronectin (Vtn), mRNA. 11/22Length = 1588	vitronectin

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2027	20440	NM_019166	b,l,m	Rattus norvegicus synaptogyrin 1 (Syngr1), mRNA. 11/22Length = 879	synaptogyrin 1
2028	7486	NM_019169	n,o	Rattus norvegicus synuclein, alpha (Snca), mRNA. 11/22Length = 118	synuclein, alpha
2029	17063	NM_019170	f,g	Rattus norvegicus carbonyl reductase 1 (Cbr1), mRNA. 11/22Length = 118	carbonyl reductase 1
2029	17064	NM_019170	f,g	Rattus norvegicus carbonyl reductase 1 (Cbr1), mRNA. 11/22Length = 118	carbonyl reductase 1
2029	17066	NM_019170	g	Rattus norvegicus carbonyl reductase 1 (Cbr1), mRNA. 11/22Length = 118	carbonyl reductase 1
2030	1174	NM_019184	c	Rattus norvegicus Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase) (Cyp2c), mRNA. 11/22Length = 1856	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
2031	23481	NM_019185	aa,bb	Rattus norvegicus GATA-binding protein 6 (Gata6), mRNA. 3/21Length = 1844	GATA-binding protein 6
2032	24019	NM_019186	j,k	Rattus norvegicus ADP-ribosylation-like 4 (Arl4), mRNA. 11/22Length = 167	ADP-ribosylation-like 4
2033	15244	NM_019191	ll	Rattus norvegicus MAD homolog 2 (Drosophila) (Madh2), mRNA. 11/22Length = 2113	MAD homolog 2 (Drosophila)
2034	21421	NM_019196	ll	Rattus norvegicus multiple PDZ domain protein (Mpdz), mRNA. 11/22Length = 7516	multiple PDZ domain protein
2035	18572	NM_019201	n,o	Rattus norvegicus C-terminal binding protein 1 (Ctbp1), mRNA. 11/22Length = 243	C-terminal binding protein 1
2035	18573	NM_019201	f,g	Rattus norvegicus C-terminal binding protein 1 (Ctbp1), mRNA. 11/22Length = 243	C-terminal binding protein 1
2036	21508	NM_019208	ii	Rattus norvegicus multiple endocrine neoplasia 1 (Men1), mRNA. 11/22Length = 367	multiple endocrine neoplasia 1
2037	18569	NM_019212	f,w,x,hh	Rattus norvegicus actin alpha 1 (Acta1), mRNA. 1/22Length = 1134	actin, alpha 1, skeletal muscle
2038	2632	NM_019213	cc,dd	Rattus norvegicus jumping translocation breakpoint (Jtb), mRNA. 11/22Length = 897	jumping translocation breakpoint
2039	2079	NM_019220	c	Rattus norvegicus amino-terminal enhancer of split (Aes), mRNA. 1/22Length = 1356	amino-terminal enhancer of split
2040	15347	NM_019222	ll	Rattus norvegicus coronin, actin-binding protein, 1B(Coro1b), mRNA. 11/22Length = 18	coronin, actin binding protein 1B

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SEQ.ID	GLGC.ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2041	20938	NM_019223	hh	Rattus norvegicus NADH dehydrogenase Fe-S protein 6 (Ndufs6), mRNA. 11/22Length = 351	NADH dehydrogenase Fe-S protein 6
2042	20433	NM_019232	p,q,kk	Rattus norvegicus serum/glucocorticoid regulated kinase (Sgk), mRNA. 11/22Length = 2435	serum/glucocorticoid regulated kinase
2043	15503	NM_019237	n,o	Rattus norvegicus procollagen C-proteinase enhancer protein(Pcolce), mRNA. 11/22Length = 1547	procollagen C-proteinase enhancer protein
2044	17908	NM_019242	a,p,q,y,z,bb,ee,ff	Rattus norvegicus interferon-related developmental regulator 1 (Ifrd1), mRNA. 5/22Length = 1736	interferon-related developmental regulator 1
2045	21108	NM_019243	f	Rattus norvegicus prostaglandin F2 receptor negativeregulator (Ptgfrn), mRNA. 11/22Length = 5825	prostaglandin F2 receptor negative regulator
2046	11218	NM_019247	b,u,v	Rattus norvegicus paired-like homeodomain transcription factor 3 (Pitx3), mRNA. 11/22Length = 1253	paired-like homeodomain transcription factor 3
2047	24849	NM_019248	aa,bb	Rattus norvegicus neural receptor protein-tyrosine kinase (Ntrk3), mRNA. 11/22Length = 2682	neurotrophic tyrosine kinase, receptor, type 3
2048	18761	NM_019250	aa	Rattus norvegicus ral guanine nucleotide dissociationstimulator (Ralgds), mRNA. 11/22Length = 3665	ral guanine nucleotide dissociation stimulator
2049	23419	NM_019257	t	Rattus norvegicus splicing factor, arginine/serine-rich 5 (Sfrs5), mRNA. 11/22Length = 2781	splicing factor, arginine/serine-rich 5 (SRp40, HRS)
2050	21443	NM_019262	kk,ll	Rattus norvegicus complement component 1, q subcomponent, betapolypeptide (C1qb), mRNA. 11/22Length = 1136	complement component 1, q subcomponent, beta polypeptide
2050	21444	NM_019262	jj,kk	Rattus norvegicus complement component 1, q subcomponent, betapolypeptide (C1qb), mRNA. 11/22Length = 1136	complement component 1, q subcomponent, beta polypeptide
2051	1143	NM_019280	w,x	Rattus norvegicus gap junction membrane channel protein alpha 5(Gja5), mRNA. 11/22Length = 3115	gap junction membrane channel protein alpha 5 (connexin 40)
2052	20734	NM_019283	j,k,t,u,v,jj,kk	Rattus norvegicus solute carrier family 3, member 2 (Slc3a2),mRNA. 11/22Length = 194	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
2052	20735	NM_019283	j,k,t,y,z,kk	Rattus norvegicus solute carrier family 3, member 2 (Slc3a2),mRNA. 11/22Length = 194	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
2053	8200	NM_019285	ll	Rattus norvegicus adenylyl cyclase 4 (Adcy4), mRNA. 11/22Length = 3357	Adenylyl cyclase 4

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2054	10015	NM_019289	n,o,jj,kk,ll	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA. 11/2Length = 143	Actin-related protein complex 1b
2054	10016	NM_019289	a,o,jj,kk,ll	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA. 11/2Length = 143	Actin-related protein complex 1b
2055	23679	NM_019290	p,q	Rattus norvegicus B-cell translocation gene 3 (Btg3), mRNA. 11/2Length = 1259	B-cell translocation gene 3
2056	15056	NM_019291	b,c	Rattus norvegicus carbonic anhydrase 2 (Ca2), mRNA. 11/2Length = 1459	carbonic anhydrase 2
2057	17507	NM_019299	f,g	Rattus norvegicus clathrin, heavy polypeptide (Hc) (Cltc), mRNA. 11/2Length = 671	clathrin, heavy polypeptide (Hc)
2058	24674	NM_019328	j,k	Rattus norvegicus nuclear receptor subfamily 4, group A, member 2 (Nr4a2), mRNA. 11/2Length = 22	nuclear receptor subfamily 4, group A, member 2
2059	16330	NM_019331	h,i,ll	Rattus norvegicus Proprotein convertase subtilisin/kexin type 3 (paired basic amino acid cleaving enzyme, furin, membrane associated receptor protein) (Pcsk3), mRNA. 11/2Length = 4259	Paired basic amino acid cleaving enzyme (furin)
2060	1238	NM_019333	gg	Rattus norvegicus 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (Pfkfb4), mRNA. 11/2Length = 1739	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
2061	52	NM_019335	d	Rattus norvegicus Protein kinase, interferon-inducible doublestranded RNA dependent (Prkr), mRNA. 11/2Length = 388	Protein kinase, interferon-inducible double stranded RNA dependent
2062	2088	NM_019341	aa,bb	Rattus norvegicus regulator of G-protein signaling 5 (Rgs5), mRNA. 11/2Length = 546	regulator of G-protein signaling 5
2063	22675	NM_019358	a,n,o,kk	Rattus norvegicus glycoprotein 38 (Gp38), mRNA. 11/2Length = 1854	glycoprotein 38
2064	23491	NM_019359	r	Rattus norvegicus calponin 3, acidic (Cnn3), mRNA. 5/2Length = 1932	calponin 3, acidic
2065	23225	NM_019360	c	Rattus norvegicus cytochrome oxidase subunit VIc (Cox6c), mRNA. 11/2Length = 418	cytochrome oxidase subunit VIc
2066	18819	NM_019367	l,m	Rattus norvegicus palmitoyl-protein thioesterase 2 (Ppt2), mRNA. 11/2Length = 166	palmitoyl-protein thioesterase 2

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2066	18820	NM_019367	s,t	Rattus norvegicus palmitoyl-protein thioesterase 2 (Ppt2), mRNA. 11/22Length = 166	palmitoyl-protein thioesterase 2
2067	1323	NM_019371	c,aa,bb,li	Rattus norvegicus EGL nine homolog 3 (C. elegans) (Egln3), mRNA. 11/22Length = 2825	EGL nine homolog 3 (C. elegans)
2067	1324	NM_019371	f,g,aa,bb,kk	Rattus norvegicus EGL nine homolog 3 (C. elegans) (Egln3), mRNA. 11/22Length = 2825	EGL nine homolog 3 (C. elegans)
2068	20298	NM_019374	l,m	Rattus norvegicus prodynorphin (Pdyn), mRNA. 11/22Length = 747	prodynorphin
2069	18032	NM_019380	b,l,m	Rattus norvegicus stromal cell derived factor receptor 1 (Sdfr1), mRNA. 11/22Length = 2369	stromal cell derived factor receptor 1
2070	2453	NM_019385	j,k	Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65), mRNA. 11/22Length = 2493	golgi peripheral membrane protein p65
2071	16	NM_019386	cc,dd,kk	Rattus norvegicus tissue-type transglutaminase (Tgm2), mRNA. 11/22Length = 3393	tissue-type transglutaminase
2072	904	NM_019620	p	Rattus norvegicus Kruppel associated box (KRAB) zinc finger 1(Kzf1), mRNA. 11/22Length = 194	Kruppel associated box (KRAB) zinc finger 1
2073	574	NM_019905	a,h,l,z,aa,kk,li	Rattus norvegicus calpactin I heavy chain (Anxa2), mRNA. 11/22Length = 1395	calpactin I heavy chain, hydroxyacid oxidase 3 (medium-chain), unknown Glu-Pro dipeptide repeat protein
2074	15911	NM_019907	cc,dd	Rattus norvegicus postsynaptic protein Cript (Cript), mRNA. 11/22Length = 1435	postsynaptic protein Cript
2075	18713	NM_020075	p,q,s,t	Rattus norvegicus eukaryotic initiation factor 5 (eIF-5)(Eif5), mRNA. 11/22Length = 354	eukaryotic initiation factor 5 (eIF-5)
2075	18715	NM_020075	ee,ff	Rattus norvegicus eukaryotic initiation factor 5 (eIF-5)(Eif5), mRNA. 11/22Length = 354	eukaryotic initiation factor 5 (eIF-5)
2076	13486	NM_020306	aa,bb	Rattus norvegicus a disintegrin and metalloproteinase domain17 (Adam17), mRNA. 11/22Length = 4128	a disintegrin and metalloproteinase domain 17
2077	20816	NM_021261	c	Rattus norvegicus thymosin, beta 1 (Tmsb1), mRNA. 11/22Length = 539	thymosin, beta 10
2078	15335	NM_021264	w	Rattus norvegicus ribosomal protein L35a (Rpl35a), mRNA. 11/22Length = 348	ribosomal protein L35a
2079	18729	NM_021578	r	Rattus norvegicus transforming growth factor, beta 1 (Tgfb1), mRNA. 11/22Length = 1585	transforming growth factor, beta-1

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2080	18946	NM_021584	s,t	Rattus norvegicus activity and neurotransmitter-induced early gene protein 4 (ania-4) (Ania4), mRNA. 11/22Length = 4831	activity and neurotransmitter-induced early gene protein 4 (ania-4)
2081	25445	NM_021654	r	Rattus norvegicus gap junction membrane channel protein alpha 4(Gja4), mRNA. 11/22Length = 12	Gap junction membrane channel, protein alpha 4 (connexin 37)
2082	23424	NM_021680	j,k	Rattus norvegicus neurexophilin 4 (Nxph4), mRNA. 11/22Length = 1265	ESTs, Highly similar to SYA_HUMAN Alanyl-tRNA synthetase (Alanine-tRNA ligase) (AlaRS) [H.sapiens]
2083	19661	NM_021686	n	Rattus norvegicus membrane-associated guanylatekinase-interacting protein (LOC59322), mRNA. 3/21Length = 2691	membrane-associated guanylate kinase-interacting protein
2084	19667	NM_021690	ii	Rattus norvegicus cAMP-regulated guanine nucleotide exchangefactor I (cAMP-GEFI) (Epac), mRNA. 11/2Length = 3373	cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI)
2085	22916	NM_021740	ii	Rattus norvegicus prothymosin alpha (Ptma), mRNA. 11/22Length = 1182	prothymosin alpha
2086	19710	NM_021744	a,j,k,q,hh,kk	Rattus norvegicus CD14 antigen (Cd14), mRNA. 11/22Length = 1591	CD14 antigen
2087	20035	NM_021754	a,y,z	Rattus norvegicus Nopp14 associated protein (Nap65), mRNA. 11/2Length = 198	Nopp140 associated protein
2088	17936	NM_021766	d,r,gg	Rattus norvegicus progesterone receptor membrane component 1(Pgrmc1), mRNA. 11/22Length = 1885	progesterone receptor membrane component 1
2089	22351	NM_021835	ee,ff	Rattus norvegicus Avian sarcoma virus 17 (v-jun) oncogene homolog (Jun), mRNA. 4/22Length = 2573	Avian sarcoma virus 17 (v-jun) oncogene homolog
2090	20161	NM_021836	j,k,p,q,r	Rattus norvegicus jun B proto-oncogene (Junb), mRNA. 11/22Length = 135	jun B proto-oncogene
2091	20177	NM_021867	d,jj,kk	Rattus norvegicus fibroblast growth factor 16 (Fgf16), mRNA. 11/22Length = 624	Fibroblast growth factor 16
2092	243	NM_021989	h,l,n,o,ll	Rattus norvegicus tissue inhibitor of metalloproteinase 2 (Timp2), mRNA. 11/22Length = 19	ESTs, tissue inhibitor of metalloproteinase 2
2093	17100	NM_022179	h,l,w,x,dd	Rattus norvegicus Hexokinase 3 (Hk3), mRNA. 12/2Length = 3692	Hexokinase 3
2094	23780	NM_022183	jj,kk	Rattus norvegicus topoisomerase (DNA) 2 alpha (Top2a), mRNA. 11/22Length = 652	topoisomerase (DNA) II alpha

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2095	20204	NM_022196	ee,ff,kk	Rattus norvegicus leukemia inhibitory factor (Lif), mRNA. 11/22Length = 69	leukemia inhibitory factor
2096	20225	NM_022198	b,l,m	Rattus norvegicus putative chloride channel (similar to MmClcn4-2) (LOC6586), mRNA. 12/2Length = 2244	putative chloride channel (similar to Mm Clcn4-2)
2097	20249	NM_022205	ll	Rattus norvegicus Chemokine receptor (LCR1) (Cxc4), mRNA. 5/22Length = 15	Chemokine receptor (LCR1)
2098	20450	NM_022239	b,l,m,u,v	Rattus norvegicus neuromedin (Nmu), mRNA. 11/22Length = 832	neuromedin U
2099	762	NM_022245	h,l	Rattus norvegicus cytochrome b5 (Cyb5), mRNA. 12/2Length = 751	cytochrome b5
2100	6263	NM_022251	jj,kk	Rattus norvegicus aminopeptidase A (Enpep), mRNA. 12/2Length = 475	aminopeptidase A
2101	6585	NM_022266	q,kk	Rattus norvegicus connective tissue growth factor (Ctgf), mRNA. 11/22Length = 2345	connective tissue growth factor
2102	13758	NM_022289	ll	Rattus norvegicus sorting nexin 16 (Snx16), mRNA. 12/2Length = 1773	ESTs
2103	23511	NM_022294	n,o	Rattus norvegicus ETL protein (Etl), mRNA. 12/2Length = 4274	ETL protein
2104	19423	NM_022297	u,v	Rattus norvegicus dimethylarginine dimethylaminohydrolase 1 (Ddah1), mRNA. 5/22Length = 38	dimethylarginine dimethylaminohydrolase 1
2105	17158	NM_022298	f,s,t	Rattus norvegicus alpha-tubulin (Tuba1), mRNA. 12/2Length = 1617	alpha-tubulin
2105	17160	NM_022298	b,l,m,aa	Rattus norvegicus alpha-tubulin (Tuba1), mRNA. 12/2Length = 1617	alpha-tubulin
2105	17161	NM_022298	a,z,kk	Rattus norvegicus alpha-tubulin (Tuba1), mRNA. 12/2Length = 1617	alpha-tubulin
2106	18246	NM_022300	hh	Rattus norvegicus brain acidic membrane protein (Basp1), mRNA. 12/2Length = 124	brain acidic membrane protein
2107	11454	NM_022381	d,l,m,n,o,s,t	Rattus norvegicus Proliferating cell nuclear antigen (Pcna), mRNA. 11/22Length = 116	Proliferating cell nuclear antigen
2107	11455	NM_022381	s	Rattus norvegicus Proliferating cell nuclear antigen (Pcna), mRNA. 11/22Length = 116	Proliferating cell nuclear antigen
2108	695	NM_022388	u,v	Rattus norvegicus FXD domain-containing ion transport regulator 4 (Fxyd4), mRNA. 11/22Length = 1362	corticosteroid-induced protein



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SEQ.ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2109	13480	NM_022390	l	Rattus norvegicus quinoid dihydropteridine reductase (Qdpr), mRNA. 11/22Length = 137	quinoid dihydropteridine reductase
2110	22412	NM_022392	p,q	Rattus norvegicus growth response protein (CL-6)(LOC64194), mRNA. 12/2Length = 241	growth response protein (CL-6)
2111	22499	NM_022393	a,p,q,cc,dd,ee,ff,jj,kk	Rattus norvegicus macrophage galactose N-acetyl-galactosamine specific lectin (Mgl), mRNA. 1/22Length = 1358	macrophage galactose N-acetyl-galactosamine specific lectin
2112	23061	NM_022394	s,t	Rattus norvegicus scaffold attachment factor B (Safb), mRNA. 11/22Length = 3113	scaffold attachment factor B
2113	18221	NM_022395	cc,dd	Rattus norvegicus mitochondrial processing peptidase beta (Pmpcb), mRNA. 12/2Length = 157	ESTs, Weakly similar to mitochondrial processing peptidase beta [Rattus norvegicus] [R.norvegicus], mitochondrial processing peptidase beta
2114	23705	NM_022396	e,j,k,li	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 (Gng11), mRNA. 12/2Length = 557	guanine nucleotide binding protein gamma subunit 11
2115	23300	NM_022398	jj,kk	Rattus norvegicus 2-oxoglutarate carrier (LOC6421), mRNA. 12/2Length = 946	2-oxoglutarate carrier
2116	24536	NM_022399	h,l,n,o	Rattus norvegicus calreticulin (Calr), mRNA. 11/22Length = 1882	calreticulin
2117	24643	NM_022400	b,u,v	Rattus norvegicus branched chain aminotransferase 2, mitochondrial (Bcat2), mRNA. 11/22Length = 1548	branched chain aminotransferase 2, mitochondrial
2118	20915	NM_022407	kk	Rattus norvegicus Aldehyde dehydrogenase 1, subfamily A1 (Aldh1a1), mRNA. 1/21Length = 212	Aldehyde dehydrogenase 1, subfamily A1
2119	8211	NM_022500	jj,kk	Rattus norvegicus ferritin light chain 1 (Ftl1), mRNA. 11/22Length = 552	ferritin light chain 1
2119	8212	NM_022500	h,l,kk,li	Rattus norvegicus ferritin light chain 1 (Ftl1), mRNA. 11/22Length = 552	ferritin light chain 1
2120	4259	NM_022504	f,g	Rattus norvegicus ribosomal protein L36 (Rpl36), mRNA. 11/22Length = 364	ribosomal protein L36
2121	8586	NM_022505	gg	Rattus norvegicus Rhesus blood group (Rh), mRNA. 11/22Length = 1269	Rhesus blood group
2121	8587	NM_022505	b,u,v	Rattus norvegicus Rhesus blood group (Rh), mRNA. 11/22Length = 1269	Rhesus blood group
2122	1867	NM_022510	c,kk	Rattus norvegicus ribosomal protein L4 (Rpl4), mRNA. 11/22Length = 1387	ribosomal protein L4

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2123	2109	NM_022511	n,o,w,x	Rattus norvegicus profilin (Pfn1), mRNA. 12/2Length = 689	profilin
2124	3027	NM_022514	w,x	Rattus norvegicus ribosomal protein L27 (Rpl27), mRNA. 11/22Length = 463	ribosomal protein L27
2125	2696	NM_022515	cc,dd	Rattus norvegicus ribosomal protein L24 (Rpl24), mRNA. 11/22Length = 541	ribosomal protein L24
2125	2697	NM_022515	f,g,gg	Rattus norvegicus ribosomal protein L24 (Rpl24), mRNA. 11/22Length = 541	ribosomal protein L24
2126	3900	NM_022516	s,t	Rattus norvegicus polypyrimidine tract binding protein (Ptbt), mRNA. 11/22Length = 2723	polypyrimidine tract binding protein
2126	3904	NM_022516	aa,bb,ll	Rattus norvegicus polypyrimidine tract binding protein (Ptbt), mRNA. 11/22Length = 2723	polypyrimidine tract binding protein
2126	162	NM_022516	e,u,v	Rattus norvegicus polypyrimidine tract binding protein (Ptbt), mRNA. 11/22Length = 2723	malate dehydrogenase mitochondrial
2127	4145	NM_022518	jj,kk	Rattus norvegicus ADP-ribosylation factor 1 (Arf1), mRNA. 11/22Length = 9	ADP-ribosylation factor 1
2127	4151	NM_022518	b,l,m	Rattus norvegicus ADP-ribosylation factor 1 (Arf1), mRNA. 11/22Length = 9	ADP-ribosylation factor 1
2128	4242	NM_022521	b,l,m	Rattus norvegicus ornithine aminotransferase (Oat), mRNA. 11/22Length = 1938	ornithine aminotransferase
2129	4412	NM_022523	l,m	Rattus norvegicus CD151 antigen (Cd151), mRNA. 11/22Length = 1668	CD151 antigen
2130	4601	NM_022524	l,m	Rattus norvegicus sushi-repeat-containing protein (SrpX), mRNA. 11/22Length = 1827	sushi-repeat-containing protein, X chromosome
2131	4615	NM_022525	cc,dd	Rattus norvegicus plasma glutathione peroxidase precursor (Gpxp), mRNA. 12/2Length = 134	plasma glutathione peroxidase precursor
2132	6100	NM_022531	n,o	Rattus norvegicus desmin (Des), mRNA. 11/22Length = 2169	desmin
2133	6577	NM_022532	u,v	Rattus norvegicus A-raf (Araf1), mRNA. 6/21Length = 2288	A-raf
2134	7505	NM_022534	ii	Rattus norvegicus transcobalamin II precursor (Tcn2p), mRNA. 11/22Length = 188	transcobalamin II precursor
2135	8097	NM_022536	h,l	Rattus norvegicus cyclophilin B (Ppib), mRNA. 12/2Length = 84	cyclophilin B

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2135	8098	NM_022536	ii	Rattus norvegicus cyclophilin B (Ppib), mRNA. 12/2Length = 84	cyclophilin B
2136	8596	NM_022538	II	Rattus norvegicus phosphatidate phosphohydrolase type 2a (Ppap2a), mRNA. 5/22Length = 871	phosphatidate phosphohydrolase type 2a
2136	8597	NM_022538	aa,bb,kk,ll	Rattus norvegicus phosphatidate phosphohydrolase type 2a (Ppap2a), mRNA. 5/22Length = 871	phosphatidate phosphohydrolase type 2a
2137	9240	NM_022540	j,k,w,x	Rattus norvegicus peroxiredoxin 3 (Prdx3), mRNA. 11/22Length = 1433	peroxiredoxin 3
2138	9541	NM_022542	e,r	Rattus norvegicus rhoB gene (Arhb), mRNA. 12/2Length = 2183	rhoB gene
2139	12422	NM_022546	n,o	Rattus norvegicus Death-associated like kinase (Dapkl), mRNA. 12/2Length = 1514	Death-associated like kinase
2140	21076	NM_022584	e,w,x	Rattus norvegicus thioredoxin reductase 2 (Txnrd2), mRNA. 11/22Length = 1999	thioredoxin reductase 2
2141	21062	NM_022585	gg	Rattus norvegicus ornithine decarboxylase antizyme inhibitor (Oazi), mRNA. 11/22Length = 4269	ornithine decarboxylase antizyme inhibitor
2141	21063	NM_022585	f,y,z	Rattus norvegicus ornithine decarboxylase antizyme inhibitor (Oazi), mRNA. 11/22Length = 4269	ornithine decarboxylase antizyme inhibitor
2142	20762	NM_022588	r,s,t	Rattus norvegicus metastasis associated 1 (Mta1), mRNA. 1/21Length = 2741	metastasis associated 1
2143	20925	NM_022594	g,hh	Rattus norvegicus enoyl coenzyme A hydratase 1 (Ech1), mRNA. 11/22Length = 197	Peroxisomal enoyl hydratase-like protein
2144	20959	NM_022598	d,r	Rattus norvegicus cellular nucleic acid binding protein (Cnbp), mRNA. 11/22Length = 164	cellular nucleic acid binding protein
2144	20960	NM_022598	c,e,r	Rattus norvegicus cellular nucleic acid binding protein (Cnbp), mRNA. 11/22Length = 164	cellular nucleic acid binding protein
2145	21115	NM_022602	j,k	Rattus norvegicus serine threonine kinase pim3 (Pim3), mRNA. 1/21Length = 2133	serine threonine kinase pim3
2146	21206	NM_022606	c	Rattus norvegicus protein phosphatase 2C (AF95927), mRNA. 1/21Length = 1318	protein phosphatase 2C
2147	17661	NM_022674	d,gg	Rattus norvegicus H2A histone family, member Z (H2afz), mRNA. 11/22Length = 811	H2A histone family, member Z

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2148	24564	NM_022676	f	Rattus norvegicus protein phosphatase 1, regulatory (inhibitor) subunit 1A (Ppp1r1a), mRNA. 11/22Length = 619	protein phosphatase 1, regulatory (inhibitor) subunit 1A
2149	20506	NM_022686	d	Rattus norvegicus germinal histone H4 gene (Hist4), mRNA. 1/21Length = 377	germinal histone H4 gene
2149	6121	NM_022686	d,r	Rattus norvegicus germinal histone H4 gene (Hist4), mRNA. 1/21Length = 377	ESTs, Highly similar to I48404 histone H4 (55AA) (1 is 3rd base in codon) - mouse (fragment) [M.musculus]
2150	20509	NM_022689	b,r,u,v	Rattus norvegicus synaptosomal-associated protein, 23 kD(Snap23), mRNA. 1/21Length = 633	synaptosomal-associated protein, 23 kD
2151	17586	NM_022694	w,x	Rattus norvegicus p15 coactivator (U83883), mRNA. 8/21Length = 3166	p105 coactivator
2152	17729	NM_022697	f,g,w,x,cc,dd	Rattus norvegicus ribosomal protein L28 (Rpl28), mRNA. 11/22Length = 466	ribosomal protein L28
2153	17757	NM_022698	cc,dd	Rattus norvegicus bcl-2 associated death agonist (Bad), mRNA. 1/21Length = 115	bcl-2 associated death agonist
2154	17808	NM_022699	cc,dd	Rattus norvegicus ribosomal protein L3 (Rpl3), mRNA. 11/22Length = 392	ribosomal protein L30
2155	24346	NM_022701	gg	Rattus norvegicus flotillin 1 (Flot1), mRNA. 11/22Length = 2157	flotillin 1
2156	58	NM_022715	u,v	Rattus norvegicus major vault protein (Mvp), mRNA. 11/22Length = 2756	major vault protein
2157	194	NM_022861	cc,dd	Rattus norvegicus Munc13-1 (Unc13h1), mRNA. 1/21Length = 6683	Munc13-1
2158	202	NM_022863	h,i	Rattus norvegicus iron-regulatory protein 2 (Ireb2), mRNA. 1/21Length = 377	iron-regulatory protein 2
2159	23606	NM_022867	w,x	Rattus norvegicus microtubule-associated proteins 1A/1B lightchain 3 (MPL3), mRNA. 1/21Length = 861	microtubule-associated proteins 1A/1B light chain 3
2159	23608	NM_022867	r	Rattus norvegicus microtubule-associated proteins 1A/1B lightchain 3 (MPL3), mRNA. 1/21Length = 861	microtubule-associated proteins 1A/1B light chain 3
2160	24283	NM_022869	s,t	Rattus norvegicus nucleolar phosphoprotein p13 (Nopp14), mRNA. 1/21Length = 369	nucleolar phosphoprotein p130
2161	6891	NM_022934	ee,ff	Rattus norvegicus DnaJ-like protein (Hsj2), mRNA. 11/22Length = 161	DnaJ-like protein
2162	2006	NM_022936	aa	Rattus norvegicus cytosolic epoxide hydrolase (Ephx2), mRNA. 1/21Length = 1992	cytosolic epoxide hydrolase

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2162	2008	NM_022936	w,x,aa,bb	Rattus norvegicus cytosolic epoxide hydrolase (Ephx2), mRNA. 1/21Length = 1992	cytosolic epoxide hydrolase
2163	15697	NM_022939	ll	Rattus norvegicus syntaxin 12 (Stx12), mRNA. 11/22Length = 819	syntaxin 12
2164	18098	NM_022947	l	Rattus norvegicus suppressor of K+ transport defect 3 (Skd3), mRNA. 11/22Length = 2138	suppressor of K+ transport defect 3
2165	18104	NM_022948	hh	Rattus norvegicus tricarboxylate carrier-like protein(Loc6542), mRNA. 1/21Length = 2699	tricarboxylate carrier-like protein
2166	18107	NM_022949	f,g	Rattus norvegicus ribosomal protein L14 (Rpl14), mRNA. 11/22Length = 715	ribosomal protein L14
2167	15727	NM_022953	u,v	Rattus norvegicus slit homolog 1 (Drosophila) (Slit1), mRNA. 11/22Length = 495	Slit1
2168	3337	NM_022961	a,y,z	Rattus norvegicus vacuolar protein sorting protein 33a(Vps33a), mRNA. 1/21Length = 3269	ESTs
2169	9286	NM_023027	l,m	Rattus norvegicus tRNA selenocysteine associated protein(Seap43), mRNA. 11/22Length = 864	tRNA selenocysteine associated protein
2170	23215	NM_023102	b,l,m	Rattus norvegicus casein kinase 1 gamma 2 isoform (Csnk1g2), mRNA. 2/21Length = 1572	casein kinase 1 gamma 2 isoform
2171	8269	NM_023103	b,l,m	Rattus norvegicus alpha(1)-inhibitor 3, variant I (Mug1), mRNA.2/21Length = 462	alpha(1)-inhibitor 3, variant I
2172	21238	NM_024125	p,q	Rattus norvegicus CCAAT/enhancer binding protein (C/EBP), beta (Cebpb), mRNA. 11/22Length = 148	Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5)
2172	21239	NM_024125	p,q,r,bb,ee,ff,k,k	Rattus norvegicus CCAAT/enhancer binding protein (C/EBP), beta (Cebpb), mRNA. 11/22Length = 148	Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5)
2173	352	NM_024127	p,q	Rattus norvegicus growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 11/22Length = 711	DNA-damage-inducible transcript 1
2173	353	NM_024127	q,ee,ff,gg	Rattus norvegicus growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 11/22Length = 711	DNA-damage-inducible transcript 1
2173	354	NM_024127	p,q,ee,ff	Rattus norvegicus growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 11/22Length = 711	DNA-damage-inducible transcript 1

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2174	17226	NM_024131	b,c,u,v	Rattus norvegicus D-dopachrome tautomerase (Ddt), mRNA. 11/22Length = 628	D-dopachrome tautomerase
2174	17227	NM_024131	c	Rattus norvegicus D-dopachrome tautomerase (Ddt), mRNA. 11/22Length = 628	D-dopachrome tautomerase
2175	1879	NM_024138	l,m	Rattus norvegicus guanine nucleotide binding protein, gamma 7 (Gng7), mRNA. 11/22Length = 2897	guanine nucleotide binding protein (G protein), gamma 7 subunit
2176	24623	NM_024146	ll	Rattus norvegicus Fibroblast growth factor receptor 1 (Fgfr1), mRNA. 5/22Length = 2469	Fibroblast growth factor receptor 1
2177	20801	NM_024148	d,s,t	Rattus norvegicus apurinic/aprimidinic endonuclease 1 (Apex), mRNA. 5/22Length = 1213	apurinic/aprimidinic endonuclease 1
2178	1742	NM_024150	p,q,y,ee,ff	Rattus norvegicus ADP-ribosylation factor 2 (Arf2), mRNA. 11/22Length = 17	ADP-ribosylation factor 2
2179	17517	NM_024151	f	Rattus norvegicus ADP-ribosylation factor 4 (Arf4), mRNA. 11/22Length = 168	ADP-ribosylation factor 4
2180	21696	NM_024152	y,z	Rattus norvegicus ADP-ribosylation factor 6 (Arf6), mRNA. 11/22Length = 995	ADP-ribosylation factor 6
2181	561	NM_024156	jj,kk	Rattus norvegicus annexin VI (Anxa6), mRNA. 11/22Length = 2739	annexin VI
2181	562	NM_024156	r	Rattus norvegicus annexin VI (Anxa6), mRNA. 11/22Length = 2739	annexin VI
2182	4504	NM_024159	d	Rattus norvegicus disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (Dab2), mRNA. 5/22Length = 317	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)
2183	20770	NM_024160	n,o	Rattus norvegicus cytochrome b558 alpha-subunit (Cyba), mRNA. 2/21Length = 79	cytochrome b558 alpha-subunit
2184	16476	NM_024162	aa	Rattus norvegicus fatty acid binding protein 3 (Fabp3), mRNA. 11/22Length = 666	Fatty acid binding protein 3, muscle and heart
2185	17764	NM_024351	e,p,r,ee,ff	Rattus norvegicus Heat shock cognate protein 7 (Hsc7), mRNA. 11/22Length = 273	heat shock 70kD protein 8
2185	17765	NM_024351	e,p,q,r,ee,ff	Rattus norvegicus Heat shock cognate protein 7 (Hsc7), mRNA. 11/22Length = 273	heat shock 70kD protein 8
2186	20933	NM_024353	h,i	Rattus norvegicus Phospholipase C, beta4 (Plcb4), mRNA. 1/22Length = 5297	Phospholipase C, beta4

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2187	15349	NM_024356	a,y,z	Rattus norvegicus GTP cyclohydrolase 1 (Gch), mRNA. 11/22Length = 116	GTP cyclohydrolase 1
2187	15353	NM_024356	j,k,y,z,ii	Rattus norvegicus GTP cyclohydrolase 1 (Gch), mRNA. 11/22Length = 116	GTP cyclohydrolase 1
2188	1146	NM_024359	y,z	Rattus norvegicus hypoxia inducible factor 1, alpha subunit (Hif1a), mRNA. 11/22Length = 3718	hypoxia inducible factor 1, alpha subunit
2189	767	NM_024365	b,c	Rattus norvegicus 5-hydroxytryptamine (serotonin) receptor 6(Htr6), mRNA. 11/22Length = 1929	5-hydroxytryptamine (serotonin) receptor 6
2190	15622	NM_024369	f,g	Rattus norvegicus follistatin-related protein (Frp), mRNA. 11/22Length = 137	follistatin-related protein precursor
2190	15623	NM_024369	r	Rattus norvegicus follistatin-related protein (Frp), mRNA. 11/22Length = 137	follistatin-related protein precursor
2191	23488	NM_024375	n,o	Rattus norvegicus prepro bone inducing protein (Gdf1), mRNA. 3/21Length = 2411	prepro bone inducing protein
2192	11628	NM_024383	b	Rattus norvegicus hairy and enhancer of split 5 (Drosophila)(Hes5), mRNA. 11/22Length = 592	hairy and enhancer of split 5 (Drosophila)
2193	2811	NM_024386	cc,dd	Rattus norvegicus 3-hydroxy-3-methylglutaryl CoA lyase (Hmgcl), mRNA. 3/21Length = 139	3-hydroxy-3-methylglutaryl CoA lyase
2193	2812	NM_024386	w,x,cc,dd	Rattus norvegicus 3-hydroxy-3-methylglutaryl CoA lyase (Hmgcl), mRNA. 3/21Length = 139	3-hydroxy-3-methylglutaryl CoA lyase
2193	2813	NM_024386	b	Rattus norvegicus 3-hydroxy-3-methylglutaryl CoA lyase (Hmgcl), mRNA. 3/21Length = 139	3-hydroxy-3-methylglutaryl CoA lyase
2194	21	NM_024388	w,x	Rattus norvegicus immediate early gene transcription factor NGFI-B (Nr4a1), mRNA. 3/21Length = 2488	immediate early gene transcription factor NGFI-B
2194	22	NM_024388	w,x	Rattus norvegicus immediate early gene transcription factor NGFI-B (Nr4a1), mRNA. 3/21Length = 2488	immediate early gene transcription factor NGFI-B
2195	25070	NM_024392	r,ii	Rattus norvegicus peroxisomal multifunctional enzyme type II (Hsd17b4), mRNA. 3/21Length = 2535	peroxisomal multifunctional enzyme type II
2196	22626	NM_024400	kk	Rattus norvegicus a disintegrin and metalloproteinase with thrombospondin motifs 1 (ADAMTS-1) (Adamts1), mRNA. 1/22Length = 4878	a disintegrin and metalloproteinase with thrombospondin motifs 1 (ADAMTS-1)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2197	13633	NM_024403	e,p,q,y,z	Rattus norvegicus activating transcription factor ATF-4 (Atf4), mRNA. 3/21Length = 1173	activating transcription factor ATF-4
2197	13634	NM_024403	a,j,k,p,q,y,z	Rattus norvegicus activating transcription factor ATF-4 (Atf4), mRNA. 3/21Length = 1173	activating transcription factor ATF-4
2198	938	NM_024486	u,v	Rattus norvegicus activin type I receptor (Acvr1), mRNA. 3/21Length = 178	activin type I receptor
2199	862	NM_024487	hh	Rattus norvegicus GrpE-like 1, mitochondrial (Grpel1), mRNA. 5/22Length = 961	GrpE-like 1, mitochondrial
2200	17917	NM_024488	b,v	Rattus norvegicus CDK5 activator-binding protein C53 (C53), mRNA. 3/21Length = 1865	CDK5 activator-binding protein C53
2201	348	NM_030586	u,v	Rattus norvegicus cytochrome b5, outer mitochondrial membrane isoform (omb5), mRNA. 3/21Length = 845	cytochrome b5, outer mitochondrial membrane isoform
2201	349	NM_030586	ll	Rattus norvegicus cytochrome b5, outer mitochondrial membrane isoform (omb5), mRNA. 3/21Length = 845	cytochrome b5, outer mitochondrial membrane isoform
2202	1852	NM_030826	aa,gg	Rattus norvegicus Glutathione peroxidase 1 (Gpx1), mRNA. 11/22Length = 1539	ESTs, Glutathione peroxidase 1
2203	21746	NM_030828	c	Rattus norvegicus glypican 1 (Gpc1), mRNA. 11/22Length = 359	glypican 1
2204	18023	NM_030846	b	Rattus norvegicus growth factor receptor bound protein 2 (Grb2), mRNA. 11/22Length = 299	growth factor receptor bound protein 2
2205	21509	NM_030847	h,l,n,o	Rattus norvegicus epithelial membrane protein 3 (Emp3), mRNA. 11/22Length = 737	epithelial membrane protein 3
2206	16292	NM_030860	cc,dd	Rattus norvegicus myocyte enhancer factor 2D (Mef2d), mRNA. 11/22Length = 1557	myocyte enhancer factor 2D
2207	1048	NM_030863	s,t,hh	Rattus norvegicus moesin (Msn), mRNA. 11/22Length = 299	moesin
2208	1928	NM_030872	s,t	Rattus norvegicus pyruvate dehydrogenase kinase 2 (Pdk2), mRNA. 11/22Length = 227	pyruvate dehydrogenase kinase 2 subunit p45 (PDK2)
2208	1929	NM_030872	hh	Rattus norvegicus pyruvate dehydrogenase kinase 2 (Pdk2), mRNA. 11/22Length = 227	pyruvate dehydrogenase kinase 2 subunit p45 (PDK2)
2209	21801	NM_030987	cc,dd,ii	Rattus norvegicus Guanine nucleotide-binding protein beta 1 (Gnb1), mRNA. 4/22Length = 2837	Guanine nucleotide-binding protein beta 1



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2209	21805	NM_030987	cc,dd	Rattus norvegicus Guanine nucleotide-binding protein beta 1 (Gnb1), mRNA. 4/22Length = 2837	Guanine nucleotide-binding protein beta 1
2210	8815	NM_030991	aa,bb	Rattus norvegicus synaptosomal-associated protein (Snap25), mRNA. 11/22Length = 21	ESTs, Highly similar to LAS1_MOUSE LIM AND SH3 DOMAIN PROTEIN 1 (LASP-1) (MLN 50) [M.musculus]
2211	1991	NM_030995	h,l	Rattus norvegicus Microtubule-associated protein 1a (Map1a), mRNA. 4/21Length = 1,12	Microtubule-associated protein 1a
2212	21166	NM_031005	a,n,o	Rattus norvegicus actinin, alpha 1 (Actn1), mRNA. 5/22Length = 2956	actinin, alpha 1
2213	25517	NM_031010	c,v	Rattus norvegicus arachidonate 12-lipoxygenase (Alox12), mRNA. 11/22Length = 248	arachidonate 12-lipoxygenase
2213	1845	NM_031010	c,v	Rattus norvegicus arachidonate 12-lipoxygenase (Alox12), mRNA. 11/22Length = 248	arachidonate 12-lipoxygenase
2214	15682	NM_031011	n,o	Rattus norvegicus S-Adenosylmethionine decarboxylase 1A (Amd1a), mRNA. 11/22Length = 312	S-Adenosylmethionine decarboxylase 1
2214	15683	NM_031011	cc,dd,gg	Rattus norvegicus S-Adenosylmethionine decarboxylase 1A (Amd1a), mRNA. 11/22Length = 312	S-Adenosylmethionine decarboxylase 1
2215	1540	NM_031012	n	Rattus norvegicus alanyl (membrane) aminopeptidase (Anpep), mRNA. 1/22Length = 332	alanyl (membrane) aminopeptidase
2216	1024	NM_031016	s,u,v	Rattus norvegicus muscarinic receptor m2 (Chrm2), mRNA. 4/21Length = 2483	muscarinic receptor m2
2216	1025	NM_031016	u,v	Rattus norvegicus muscarinic receptor m2 (Chrm2), mRNA. 4/21Length = 2483	muscarinic receptor m2
2217	485	NM_031017	l,m	Rattus norvegicus cAMP response element binding protein 1 (Creb1), mRNA. 3/22Length = 1125	cAMP response element binding protein 1
2218	1719	NM_031024	jj,kk	Rattus norvegicus drebrin 1 (Dbn1), mRNA. 11/22Length = 2697	drebrin 1
2219	16210	NM_031026	l,m	Rattus norvegicus LIC-2 dynein light intermediate chain 53/55(Dncll2), mRNA. 4/21Length = 43	LIC-2 dynein light intermediate chain 53/55
2220	690	NM_031034	w,x	Rattus norvegicus guanine nucleotide binding protein, alpha 12 (Gna12), mRNA. 11/22Length = 1423	guanine nucleotide binding protein (G protein) alpha 12
2221	15886	NM_031035	r,bb,ll	Rattus norvegicus GTP-binding protein (G-alpha-i2) (Gnai2), mRNA. 4/21Length = 1748	GTP-binding protein (G-alpha-i2)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2222	17727	NM_031043	c	Rattus norvegicus glycogenin (Gyg), mRNA. 11/22Length = 1624	glycogenin
2223	18188	NM_031046	gg	Rattus norvegicus inositol 1,4,5-triphosphate receptor type 2 (Itpr2), mRNA. 11/22Length = 1,78	inositol triphosphate receptor type 2
2224	1731	NM_031047	jj,kk	Rattus norvegicus uncton plakoglobin (Jup), mRNA. 4/21Length = 3177	uncton plakoglobin
2225	15957	NM_031050	c,ii	Rattus norvegicus lumican (Lum), mRNA. 11/22Length = 174	lumican
2226	21182	NM_031054	l,m	Rattus norvegicus matrix metalloproteinase 2 (72 KDa type IVcollagenase) (Mmp2), mRNA. 5/22Length = 3231	Rattus norvegicus gelatinase A mRNA, complete cds
2227	11849	NM_031065	h,i,l,n,o	Rattus norvegicus ribosomal protein L1a (Rpl1a), mRNA. 11/22Length = 71	ribosomal protein L10a
2228	25600	NM_031077	b,l,m	Rattus norvegicus PCTAIRE-1 protein kinase, alternatively spliced (Pctk1), mRNA. 1/22Length = 3111	PCTAIRE-1 protein kinase, alternatively spliced
2228	6349	NM_031077	ee,ff	Rattus norvegicus PCTAIRE-1 protein kinase, alternatively spliced (Pctk1), mRNA. 1/22Length = 3111	PCTAIRE-1 protein kinase, alternatively spliced
2229	79	NM_031079	y,z,ee,ff	Rattus norvegicus cyclic GMP stimulated phosphodiesterase (Pde2a), mRNA. 4/21Length = 398	cyclic GMP stimulated phosphodiesterase
2230	4684	NM_031083	b,l,m	Rattus norvegicus phosphatidylinositol 4-kinase (Pik4cb), mRNA. 11/22Length = 325	phosphatidylinositol 4-kinase
2231	18307	NM_031091	w,x	Rattus norvegicus Rab3B protein (Rab3b), mRNA. 4/21Length = 66	Rab3B protein
2231	18308	NM_031091	w,x	Rattus norvegicus Rab3B protein (Rab3b), mRNA. 4/21Length = 66	Rab3B protein
2232	15201	NM_031093	h,i,l,w	Rattus norvegicus (Rala), mRNA. 11/22Length = 952	
2232	15202	NM_031093	f,w,x,cc,dd	Rattus norvegicus(Rala), mRNA. 11/22Length = 952	
2232	15203	NM_031093	aa,bb	Rattus norvegicus (Rala), mRNA. 11/22Length = 952	
2233	1376	NM_031094	ii	Rattus norvegicus Retinoblastoma-related gene (Rb2), mRNA. 11/22Length = 4861	Retinoblastoma-related gene
2234	1295	NM_031097	j,k,r	Rattus norvegicus aminopeptidase B (Rnpep), mRNA. 4/21Length = 228	aminopeptidase B
2235	12638	NM_031099	e	Rattus norvegicus ribosomal protein L5 (Rpl5), mRNA. 11/22Length = 169	ribosomal protein L5

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2235	12639	NM_031099	g	Rattus norvegicus ribosomal protein L5 (Rpl5), mRNA. 11/22Length = 169	ribosomal protein L5
2236	20812	NM_031100	g,h,l	Rattus norvegicus ribosomal protein L1 (Rpl1), mRNA. 11/22Length = 769	ribosomal protein L10
2237	23854	NM_031101	f,w,x,ll	Rattus norvegicus ribosomal protein L13 (Rpl13), mRNA. 11/22Length = 722	ribosomal protein L13
2238	20462	NM_031102	h,l	Rattus norvegicus ribosomal protein L18 (Rpl18), mRNA. 11/22Length = 67	ribosomal protein L18
2239	16938	NM_031103	g	Rattus norvegicus ribosomal protein L19 (Rpl19), mRNA. 11/22Length = 73	ribosomal protein L19
2240	22205	NM_031105	b	Rattus norvegicus large subunit ribosomal protein L36a(Rpl36a), mRNA. 4/21Length = 444	large subunit ribosomal protein L36a
2241	20807	NM_031106	f,g	Rattus norvegicus ribosomal protein L37 (Rpl37), mRNA. 11/22Length = 366	ribosomal protein L37
2242	16847	NM_031109	h,l,x	Rattus norvegicus ribosomal protein S1 (Rps1), mRNA. 11/22Length = 61	ribosomal protein S10
2243	10878	NM_031110	g,j,k	Rattus norvegicus ribosomal protein S11 (Rps11), mRNA. 11/22Length = 534	ribosomal protein S11
2244	19162	NM_031111	h,l	Rattus norvegicus ribosomal protein S21 (Rps21), mRNA. 11/22Length = 359	ribosomal protein S21
2245	25458	NM_031112	h,l	Rattus norvegicus ribosomal protein S24 (Rps24), mRNA. 11/22Length = 466	
2246	20839	NM_031113	w,x	Rattus norvegicus ribosomal protein S27a (Rps27a), mRNA. 4/21Length = 552	ribosomal protein S27a
2247	19040	NM_031114	a,c,h,l,y,ee,ff	Rattus norvegicus S-1 related protein, clone 42C (S1A1), mRNA. 2/22Length = 573	S-100 related protein, clone 42C
2248	23568	NM_031122	e	Rattus norvegicus suppression of tumorigenicity 13 (coloncarcinoma) Hsp7-interacting protein (St13), mRNA. 4/21Length = 1694	suppression of tumorigenicity 13 (colon carcinoma) Hsp70-interacting protein
2248	23569	NM_031122	r	Rattus norvegicus suppression of tumorigenicity 13 (coloncarcinoma) Hsp7-interacting protein (St13), mRNA. 4/21Length = 1694	suppression of tumorigenicity 13 (colon carcinoma) Hsp70-interacting protein
2249	882	NM_031123	d	Rattus norvegicus stanniocalcin 1 (Stc1), mRNA. 11/22Length = 14	stanniocalcin 1
2250	1265	NM_031124	u,v	Rattus norvegicus syntaxin 3 (Stx3a), mRNA. 11/22Length = 154	syntaxin 3
2251	14970	NM_031127	a,h,l,n,o	Rattus norvegicus sulfite oxidase (Suox), mRNA. 11/22Length = 1777	sulfite oxidase

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2252	6525	NM_031129	gg	Rattus norvegicus transcription elongation factor B (SIII) polypeptide 2 (18kD, elongin B) (TCEB2), mRNA. 4/21Length = 357	transcription elongation factor B (SIII) polypeptide 2 (18kD, elongin B)
2253	13929	NM_031131	n,o,hh	Rattus norvegicus transforming growth factor, beta 2 (Tgfb2), mRNA. 11/22Length = 288	TGF beta 2 protein
2254	1816	NM_031134	l,m	Rattus norvegicus thyroid hormone receptor alpha (Thra), mRNA. 11/22Length = 246	thyroid hormone receptor alpha
2255	13358	NM_031135	d	Rattus norvegicus TGFB inducible early growth response (Tieg), mRNA. 11/22Length = 3115	TGFB inducible early growth response
2255	13359	NM_031135	s,t	Rattus norvegicus TGFB inducible early growth response (Tieg), mRNA. 11/22Length = 3115	TGFB inducible early growth response
2256	15052	NM_031136	c,w,x,aa,bb	Rattus norvegicus thymosin beta-4 (Tmsb4x), mRNA. 4/21Length = 686	thymosin beta-4
2256	19359	NM_031136	h,l	Rattus norvegicus thymosin beta-4 (Tmsb4x), mRNA. 4/21Length = 686	EST
2257	15485	NM_031137	l,m	Rattus norvegicus tripeptidylpeptidase II (Tpp2), mRNA. 4/21Length = 4566	tripeptidylpeptidase II
2257	15486	NM_031137	w,x	Rattus norvegicus tripeptidylpeptidase II (Tpp2), mRNA. 4/21Length = 4566	tripeptidylpeptidase II
2258	17379	NM_031138	r,w,x	Rattus norvegicus ubiquitin conjugating enzyme (LOC81816), mRNA. 4/21Length = 1737	ubiquitin conjugating enzyme
2259	15185	NM_031140	n,bb,ll	Rattus norvegicus vimentin (Vim), mRNA. 11/22Length = 1796	vimentin
2260	1638	NM_031143	d,e,ii,kk	Rattus norvegicus diacylglycerol kinase zeta (Dgkz), mRNA. 11/22Length = 356	diacylglycerol kinase zeta
2261	21623	NM_031144	c	Rattus norvegicus cytoplasmic beta-actin (Actx), mRNA. 4/21Length = 1128	
2262	23097	NM_031145	n,o,cc,dd	Rattus norvegicus calcium- and integrin-binding protein (Sip2-28), mRNA. 4/21Length = 822	calcium- and integrin-binding protein
2263	1291	NM_031149	c,r	Rattus norvegicus for proteasomal ATPase (SUG1) (LOC81827), mRNA. 4/21Length = 1288	for proteasomal ATPase (SUG1)
2264	239	NM_031152	e	Rattus norvegicus RAB11a, member RAS oncogene family (Rab11a), mRNA. 11/22Length = 895	RAB11a, member RAS oncogene family

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2265	20862	NM_031154	w,x	Rattus norvegicus glutathione S-transferase, mu type 3 (Yb3) (Gstm3), mRNA. 4/21Length = 128	glutathione S-transferase, mu type 3 (Yb3)
2266	15273	NM_031237	aa,bb	Rattus norvegicus ubiquitin-conjugating enzyme E2D 3(homologous to yeast UBC4/5) (Ube2d3), mRNA. 4/21Length = 1531	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
2266	15277	NM_031237	a	Rattus norvegicus ubiquitin-conjugating enzyme E2D 3(homologous to yeast UBC4/5) (Ube2d3), mRNA. 4/21Length = 1531	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
2267	18596	NM_031325	u,v	Rattus norvegicus UDP-glucose dehydrogeanse (Ugdh), mRNA.4/21Length = 2318	UDP-glucose dehydrogeanse
2267	18597	NM_031325	a,j,k,p,q,y,z,ee,ff	Rattus norvegicus UDP-glucose dehydrogeanse (Ugdh), mRNA.4/21Length = 2318	UDP-glucose dehydrogeanse
2268	11258	NM_031327	y,z,ee,ff,gg	Rattus norvegicus cysteine rich protein 61 (Cyr61), mRNA. 11/22Length = 1871	cysteine rich protein 61
2269	4235	NM_031330	b,d,f,g,l,m	Rattus norvegicus heterogeneous nuclear ribonucleoprotein A/B(Hnrapab), mRNA. 11/22Length = 361	heterogeneous nuclear ribonucleoprotein A/B
2270	18539	NM_031353	f,g	Rattus norvegicus voltage-dependent anion channel 1 (Vdac1), mRNA. 11/22Length = 1818	voltage-dependent anion channel 1
2271	16777	NM_031354	hh	Rattus norvegicus voltage-dependent anion channel 2 (Vdac2), mRNA. 11/22Length = 1715	voltage-dependent anion channel 2
2272	20087	NM_031357	cc,dd	Rattus norvegicus ceroid-lipofuscinosis, neuronal 2 (Cln2),mRNA. 11/22Length = 2485	ESTs
2273	18654	NM_031358	a,d,r,y,z,ee,ff,k,k	Rattus norvegicus potassium inwardly rectifying channel,subfamily J, member 11 (Kcnj11), mRNA. 11/22Length = 335	potassium inwardly-rectifying channel, subfamily J, member 11
2273	18655	NM_031358	d,l,m,jj,kk	Rattus norvegicus potassium inwardly rectifying channel,subfamily J, member 11 (Kcnj11), mRNA. 11/22Length = 335	potassium inwardly-rectifying channel, subfamily J, member 11
2274	25525	NM_031509	b,r	Rattus norvegicus Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. 5/21Length = 1178	Glutathione-S-transferase, alpha type (Ya)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2274	634	NM_031509	d,r	Rattus norvegicus Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. 5/21Length = 1178	Glutathione-S-transferase, alpha type (Ya)
2274	635	NM_031509	d,r	Rattus norvegicus Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. 5/21Length = 1178	Glutathione-S-transferase, alpha type (Ya)
2275	17427	NM_031510	b,u,v	Rattus norvegicus Isocitrate dehydrogenase 1, soluble (Idh1),mRNA. 5/21Length = 1719	Isocitrate dehydrogenase 1, soluble
2276	12580	NM_031514	a,h,i,j,k,y,z	Rattus norvegicus Janus kinase 2 (a protein tyrosine kinase)(Jak2), mRNA. 5/21Length = 3731	Janus kinase 2 (a protein tyrosine kinase)
2276	12581	NM_031514	y,z,hh	Rattus norvegicus Janus kinase 2 (a protein tyrosine kinase)(Jak2), mRNA. 5/21Length = 3731	Janus kinase 2 (a protein tyrosine kinase)
2277	20448	NM_031530	a,d,z,ee,ff,jj,kk	Rattus norvegicus small inducible cytokine A2 (Scya2), mRNA. 11/22Length = 78	Small inducible gene JE
2277	20449	NM_031530	a,z,ee,ff,kk	Rattus norvegicus small inducible cytokine A2 (Scya2), mRNA. 11/22Length = 78	Small inducible gene JE
2278	3292	NM_031531	a,j,k	Rattus norvegicus Serine protease inhibitor (Spin2c), mRNA.11/22Length = 261	Serine protease inhibitor
2279	1005	NM_031537	l,m	Rattus norvegicus Solute carrier family 11 member 1 (Slc11a1), mRNA. 11/22Length = 167	Solute carrier family 11 member 1 (natural resistance-associated macrophage protein 1), see also D9Arb3
2280	16049	NM_031541	n,o	Rattus norvegicus CD36 antigen (collagen type I receptor,thrombospondin receptor)-like 1 (Cd361), mRNA. 1/22Length = 2497	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 (scavenger receptor class B type 1)
2281	4010	NM_031543	u,v	Rattus norvegicus Cytochrome P45, subfamily 2e1(ethanol-inducible) (Cyp2e1), mRNA. 11/22Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)
2281	4011	NM_031543	v	Rattus norvegicus Cytochrome P45, subfamily 2e1(ethanol-inducible) (Cyp2e1), mRNA. 11/22Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)
2282	18389	NM_031545	a,d,y,ee,ff	Rattus norvegicus natriuretic peptide precursor type B (Nppb),mRNA. 11/22Length = 628	Brain natriuretic factor
2283	1822	NM_031553	li	Rattus norvegicus nuclear transcription factor - Y beta (Nfyb),mRNA. 11/22Length = 734	CCAAT binding transcription factor of CBF-B/NFY-B

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2284	25795	NM_031556	jj,kk	Rattus norvegicus Caveolin, caveolae protein, 22 kDa (Cav), mRNA. 11/22Length = 537	Caveolin, caveolae protein, 22 kDa
2285	692	NM_031557	s,t,ll	Rattus norvegicus Prostaglandin I2 (prostacyclin) synthase (Ptgis), mRNA. 11/22Length = 1618	Prostaglandin I2 (prostacyclin) synthase
2286	18315	NM_031561	e,u	Rattus norvegicus cd36 antigen (Cd36), mRNA. 11/22Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
2286	18316	NM_031561	e	Rattus norvegicus cd36 antigen (Cd36), mRNA. 11/22Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
2286	18317	NM_031561	r,aa,bb,ii	Rattus norvegicus cd36 antigen (Cd36), mRNA. 11/22Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
2286	18319	NM_031561	w,x	Rattus norvegicus cd36 antigen (Cd36), mRNA. 11/22Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
2287	9620	NM_031570	w,x,cc,dd	Rattus norvegicus ribosomal protein S7 (Rps7), mRNA. 11/22Length = 65	ribosomal protein S7
2288	546	NM_031573	h,ii	Rattus norvegicus Phosphorylase kinase, gamma 1 (Phkg1), mRNA. 11/21Length = 1388	Phosphorylase kinase, gamma 1
2289	1918	NM_031576	gg	Rattus norvegicus P45 (cytochrome) oxidoreductase (Por), mRNA. 11/22Length = 2441	P450 (cytochrome) oxidoreductase
2289	1920	NM_031576	s	Rattus norvegicus P45 (cytochrome) oxidoreductase (Por), mRNA. 11/22Length = 2441	P450 (cytochrome) oxidoreductase
2289	1921	NM_031576	j,k,s,t	Rattus norvegicus P45 (cytochrome) oxidoreductase (Por), mRNA. 11/22Length = 2441	P450 (cytochrome) oxidoreductase
2290	942	NM_031577	u	Rattus norvegicus growth hormone releasing hormone (Ghrh), mRNA. 11/22Length = 616	growth hormone releasing hormone
2290	25793	NM_031577	ii	Rattus norvegicus growth hormone releasing hormone (Ghrh), mRNA. 11/22Length = 616	
2291	21715	NM_031578	aa	Rattus norvegicus testis specific protein kinase 1 (Tesk1), mRNA. 11/22Length = 3581	testis specific protein kinase 1
2292	24219	NM_031579	d,p,q,y,z,kk	Rattus norvegicus protein tyrosine phosphatase 4a1 (Ptp4a1), mRNA. 11/22Length = 2638	protein tyrosine phosphatase 4a1
2293	5496	NM_031589	a,ee,ff	Rattus norvegicus glucose-6-phosphatase, transport protein 1 (G6pt1), mRNA. 11/22Length = 193	glucose-6-phosphatase, transport protein 1

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2293	5497	NM_031589	ii	Rattus norvegicus glucose-6-phosphatase, transport protein 1 (G6pt1), mRNA. 11/22Length = 193	glucose-6-phosphatase, transport protein 1
2294	14542	NM_031596	r	Rattus norvegicus squamous cell carcinoma antigen recognized by T-cells 1 (Sart1), mRNA. 11/22Length = 2532	squamous cell carcinoma antigen recognized by T-cells
2294	14543	NM_031596	b,u,v	Rattus norvegicus squamous cell carcinoma antigen recognized by T-cells 1 (Sart1), mRNA. 11/22Length = 2532	squamous cell carcinoma antigen recognized by T-cells
2295	19341	NM_031603	h,l	Rattus norvegicus tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide (Ywhae), mRNA. 11/22Length = 1771	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
2296	20840	NM_031604	cc,dd	Rattus norvegicus ATPase, H <sup>+</sup> transporting, lysosomal noncatalytic accessory protein 1a (Atp6n1a), mRNA. 11/22Length = 3876	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) noncatalytic accessory protein 1 (110/160 kDa)
2297	11296	NM_031606	f	Rattus norvegicus phosphatase and tensin homolog (Pten), mRNA. 11/22Length = 1212	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
2298	19022	NM_031609	s,t,jj,kk	Rattus norvegicus neuroblastoma, suppression of tumorigenicity1 (Nbl1), mRNA. 11/22Length = 1788	Neuroblastoma, suppression of tumorigenicity 1 (DNA segment human D1S1733E)
2299	24234	NM_031614	r,y,z,jj,kk	Rattus norvegicus thioredoxin reductase 1 (Txnrd1), mRNA. 11/22Length = 336	thioredoxin reductase 1
2299	24235	NM_031614	y,z,kk	Rattus norvegicus thioredoxin reductase 1 (Txnrd1), mRNA. 11/22Length = 336	thioredoxin reductase 1
2300	14957	NM_031622	f	Rattus norvegicus mitogen-activated protein kinase 6 (Mapk6), mRNA. 11/22Length = 3662	mitogen-activated protein kinase 6
2301	15767	NM_031623	aa,bb,jj,kk,ll	Rattus norvegicus growth factor receptor bound protein 14 (Grb14), mRNA. 11/22Length = 195	growth factor receptor bound protein 14
2302	21772	NM_031624	y,z	Rattus norvegicus immunoglobulin binding protein 1 (Igbp1), mRNA. 11/22Length = 1239	immunoglobulin (CD79A) binding protein 1
2303	567	NM_031628	p,q	Rattus norvegicus nuclear receptor subfamily 4, group A, member 3 (Nr4a3), mRNA. 11/22Length = 44	nuclear receptor subfamily 4, group A, member 3
2304	1727	NM_031642	jj,kk	Rattus norvegicus core promoter element binding protein (Copeb), mRNA. 11/22Length = 1356	core promoter element binding protein



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2305	16062	NM_031646	n,o	Rattus norvegicus receptor (calcitonin) activity modifying protein 2 (Ramp2), mRNA. 11/22Length = 751	receptor (calcitonin) activity modifying protein 2
2306	17448	NM_031668	h,l	Rattus norvegicus MYB binding protein 1a (Mybbp1a), mRNA. 11/22Length = 3834	MYB binding protein (P160) 1a
2307	5358	NM_031675	r	Rattus norvegicus actinin alpha 4 (Actn4), mRNA. 11/22Length = 2996	Actinin, alpha 4
2308	19909	NM_031676	ii	Rattus norvegicus transgelin 3 (Tagln3), mRNA. 1/22Length = 12	EST
2309	18403	NM_031677	d,jj,kk	Rattus norvegicus four and a half LIM domains 2 (Fhl2), mRNA. 11/22Length = 84	four and a half LIM domains 2
2310	15041	NM_031678	jj,kk	Rattus norvegicus period homolog 2 (Per2), mRNA. 11/22Length = 5761	period homolog 2 (Drosophila)
2311	20743	NM_031684	a,x,z,kk	Rattus norvegicus solute carrier family 29, member 1 (Slc29a1), mRNA. 11/22Length = 1766	solute carrier family 29 (nucleoside transporters), member 1
2312	8844	NM_031690	b	Rattus norvegicus crystallin, beta B3 (Crybb3), mRNA. 11/22Length = 747	crystallin, beta B3
2313	16663	NM_031695	s	Rattus norvegicus sialyltransferase 5 (Siat5), mRNA. 11/22Length = 2725	sialyltransferase 5
2314	21575	NM_031698	w,x	Rattus norvegicus ribophorin 2 (Rpn2), mRNA. 1/22Length = 2234	ribophorin II
2315	16204	NM_031706	f,g,jj,kk	Rattus norvegicus ribosomal protein S8 (Rps8), mRNA. 11/22Length = 696	ribosomal protein S8
2315	16205	NM_031706	jj,kk	Rattus norvegicus ribosomal protein S8 (Rps8), mRNA. 11/22Length = 696	ribosomal protein S8
2316	18054	NM_031707	f,g,n,o	Rattus norvegicus homer, neuronal immediate early gene, 1(Homer1), mRNA. 11/22Length = 45	RuvB-like protein 1
2316	18057	NM_031707	r	Rattus norvegicus homer, neuronal immediate early gene, 1(Homer1), mRNA. 11/22Length = 45	RuvB-like protein 1
2316	18059	NM_031707	p,q,ee,ff	Rattus norvegicus homer, neuronal immediate early gene, 1(Homer1), mRNA. 11/22Length = 45	RuvB-like protein 1
2317	24081	NM_031708	e	Rattus norvegicus adhesion regulating molecule 1 (Adrm1), mRNA. 11/22Length = 1444	glycoprotein 110
2318	16918	NM_031709	g,h,i,w,x	Rattus norvegicus ribosomal protein S12 (Rps12), mRNA. 11/22Length = 499	ribosomal protein S12
2319	20210	NM_031710	u,v	Rattus norvegicus olfactory receptor 41 (Olf41), mRNA. 11/22Length = 984	olfactory receptor 41

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2320	1340	NM_031715	jj,kk	Rattus norvegicus phosphofructokinase, muscle (Pfk <sub>m</sub> ), mRNA. 11/22Length = 2757	phosphofructokinase, muscle
2321	19048	NM_031719	jj,kk	Rattus norvegicus chloride channel, nucleotide-sensitive, 1A(Cl <sub>ns1a</sub> ), mRNA. 11/22Length = 1399	chloride channel, nucleotide-sensitive, 1A
2322	15507	NM_031735	u	Rattus norvegicus serine/threonine kinase 3 (Stk3), mRNA. 11/22Length = 261	serine/threonine kinase 3 (Ste20, yeast homolog) STK3
2323	20724	NM_031753	d	Rattus norvegicus activated leukocyte cell adhesion molecule (A <sub>lc</sub> am), mRNA. 11/22Length = 2866	activated leukocyte cell adhesion molecule
2324	16003	NM_031757	c	Rattus norvegicus matrix metalloproteinase 24 (membrane-inserted) (Mmp24), mRNA. 11/22Length = 4245	matrix metalloproteinase 24 (membrane-inserted)
2325	14184	NM_031776	kk	Rattus norvegicus guanine deaminase (Gda), mRNA. 11/22Length = 1568	guanine deaminase
2325	14185	NM_031776	kk	Rattus norvegicus guanine deaminase (Gda), mRNA. 11/22Length = 1568	guanine deaminase
2326	4325	NM_031784	d	Rattus norvegicus potassium channel regulatory protein KChAP (83614), mRNA. 12/21Length = 2927	potassium channel regulatory protein KChAP
2327	16178	NM_031785	f	Rattus norvegicus ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump), subunit 1 (Atp6s1), mRNA. 5/21Length = 289	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump), subunit 1
2328	1169	NM_031789	d	Rattus norvegicus NF-E2-related factor 2 (Nfe2l2), mRNA. 5/21Length = 237	NF-E2-related factor 2
2328	1170	NM_031789	d,l,m,jj,kk	Rattus norvegicus NF-E2-related factor 2 (Nfe2l2), mRNA. 5/21Length = 237	NF-E2-related factor 2
2329	1182	NM_031790	b,l,m	Rattus norvegicus citron (Cit), mRNA. 11/22Length = 5952	postsynaptic density protein (citron)
2330	15864	NM_031797	r	Rattus norvegicus kangai 1 (Kai1), mRNA. 11/22Length = 174	ESTs, Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))
2331	2114	NM_031798	aa,bb	Rattus norvegicus solute carrier family 12, member 2 (Slc12a2), mRNA. 11/22Length = 642	solute carrier family 12, member 2
2332	16155	NM_031810	ii	Rattus norvegicus defensin beta 1 (Defb1), mRNA. 5/22Length = 416	defensin beta 1
2333	15840	NM_031817	h,l	Rattus norvegicus osteomodulin (osteoaderin) (Omd), mRNA. 5/21Length = 1536	osteomodulin (osteoaderin)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2334	2655	NM_031821	d	Rattus norvegicus serum-inducible kinase (Snk), mRNA. 11/22Length = 2781	serum-inducible kinase
2335	22321	NM_031832	a,h,i,n,o,x,kk	Rattus norvegicus lectin, galactose binding, soluble 3(Lgals3), mRNA. 5/22Length = 948	lectin, galactose binding, soluble 3
2336	4748	NM_031834	s,t,aa,bb	Rattus norvegicus sulfotransferase family 1A, phenol-preferring, member 1 (Sult1a1), mRNA. 1/22Length = 1227	sulfotransferase family 1A, phenol-preferring, member 1
2336	4749	NM_031834	t,bb	Rattus norvegicus sulfotransferase family 1A, phenol-preferring, member 1 (Sult1a1), mRNA. 1/22Length = 1227	Aryl sulfotransferase cytosolic, 1A, phenol-preferring, member 3, sulfotransferase family 1A, phenol-preferring, member 1
2337	8384	NM_031836	gg,il	Rattus norvegicus vascular endothelial growth factor (Vegf),mRNA. 11/22Length = 645	vascular endothelial growth factor
2337	8385	NM_031836	s,t,gg	Rattus norvegicus vascular endothelial growth factor (Vegf),mRNA. 11/22Length = 645	vascular endothelial growth factor
2337	8386	NM_031836	ll	Rattus norvegicus vascular endothelial growth factor (Vegf),mRNA. 11/22Length = 645	vascular endothelial growth factor
2338	10269	NM_031838	h,i,w,x	Rattus norvegicus ribosomal protein S2 (Rps2), mRNA. 11/22Length = 817	ribosomal protein S2
2339	15077	NM_031841	ii	Rattus norvegicus stearoyl-Coenzyme A desaturase 2 (Scd2),mRNA. 5/22Length = 555	Rat DNA polymerase alpha mRNA, 3' end, stearoyl-Coenzyme A desaturase 2
2340	19190	NM_031969	h,i	Rattus norvegicus Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. 11/22Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
2340	19191	NM_031969	h,i	Rattus norvegicus Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. 11/22Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
2340	19195	NM_031969	h,i,ll	Rattus norvegicus Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. 11/22Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
2340	25802	NM_031969	h,i,aa,bb,ll	Rattus norvegicus Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. 11/22Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
2341	17734	NM_031970	a,o,q,ee,ff,kk	Rattus norvegicus Heat shock 27 kDa protein (Hsp27), mRNA. 11/22Length = 787	ESTs, Moderately similar to hypothetical protein MGC10974 [Homo sapiens] [H.sapiens], heat shock 27kD protein 1
2341	17735	NM_031970	a,z,ee,ff,kk	Rattus norvegicus Heat shock 27 kDa protein (Hsp27), mRNA. 11/22Length = 787	ESTs, Moderately similar to hypothetical protein MGC10974 [Homo sapiens] [H.sapiens], heat shock 27kD protein 1

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2341	17736	NM_031970	a,l,o,q,ee,ff,kk	Rattus norvegicus Heat shock 27 kDa protein (Hsp27), mRNA. 11/22Length = 787	ESTs, Moderately similar to hypothetical protein MGC10974 [Homo sapiens] [H.sapiens], heat shock 27kD protein 1
2342	1475	NM_031971	a,p,q,ee,ff	Rattus norvegicus Heat shock protein 7-1 (Hspa1a), mRNA.5/21Length = 2455	ESTs, Highly similar to S10A_RAT S-100 protein, alpha chain [R.norvegicus], Heat shock protein 70-1
2342	8661	NM_031971	e,ee,ff,gg	Rattus norvegicus Heat shock protein 7-1 (Hspa1a), mRNA.5/21Length = 2455	Heat shock protein 70-1
2342	8662	NM_031971	ee,ff,gg	Rattus norvegicus Heat shock protein 7-1 (Hspa1a), mRNA.5/21Length = 2455	Heat shock protein 70-1
2342	8663	NM_031971	ee,ff,gg	Rattus norvegicus Heat shock protein 7-1 (Hspa1a), mRNA.5/21Length = 2455	Heat shock protein 70-1
2343	24644	NM_031972	cc,dd	Rattus norvegicus Aldehyde dehydrogenase family 3, subfamily A1 (Aldh3a1), mRNA. 11/22Length = 1725	Aldehyde dehydrogenase class 3
2344	17075	NM_031974	gg	Rattus norvegicus clathrin, light polypeptide (Lca) (Cita),mRNA. 11/22Length = 1124	clathrin light chain
2345	17556	NM_031975	j,k	Rattus norvegicus parathymosin (Ptms), mRNA. 11/22Length = 936	parathymosin
2346	17601	NM_031976	a,jj,kk	Rattus norvegicus protein kinase, AMP-activated, beta 1non-catalytic subunit (Prkab1), mRNA. 11/22Length = 1978	5'-AMP-activated protein kinase, beta subunit
2347	18499	NM_031984	aa,bb	Rattus norvegicus calbindin 1 (Calb1), mRNA. 11/22Length = 228	cerebellar Ca-binding protein, spot 35 protein
2347	18500	NM_031984	bb	Rattus norvegicus calbindin 1 (Calb1), mRNA. 11/22Length = 228	cerebellar Ca-binding protein, spot 35 protein
2348	18898	NM_031985	ii	Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287	S6 kinase
2348	18899	NM_031985	gg	Rattus norvegicus S6 kinase (Rps6kb1), mRNA. 5/21Length = 2287	S6 kinase
2349	19768	NM_031986	f,g,cc,dd	Rattus norvegicus syntenin (Sdcbp), mRNA. 5/21Length = 277	syntenin
2350	20554	NM_031987	b,l,m,aa,cc,dd	Rattus norvegicus carnitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681	carnitine O-octanoyltransferase
2350	20555	NM_031987	j,k	Rattus norvegicus carnitine O-octanoyltransferase (Crot), mRNA.11/22Length = 2681	carnitine O-octanoyltransferase
2351	21807	NM_032067	gg	Rattus norvegicus RalA binding protein 1 (Ralbp1), mRNA.5/21Length = 3622	RalA binding protein 1
2351	21809	NM_032067	ll	Rattus norvegicus RalA binding protein 1 (Ralbp1), mRNA.5/21Length = 3622	RalA binding protein 1

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2352	1171	NM_032071	y,z	Rattus norvegicus synaptotagmin 2 (Synj2), mRNA. 11/22Length = 533	synaptotagmin II
2353	12299	NM_032416	c	Rattus norvegicus aldehyde dehydrogenase 2 (Aldh2), mRNA. 11/22Length = 1889	aldehyde dehydrogenase 2, mitochondrial
2354	21102	NM_033021	ll	Rattus norvegicus vesicle associated protein (VAP1), mRNA. 7/21Length = 4422	vesicle associated protein
2354	21103	NM_033021	s	Rattus norvegicus vesicle associated protein (VAP1), mRNA. 7/21Length = 4422	vesicle associated protein
2354	21104	NM_033021	s,t	Rattus norvegicus vesicle associated protein (VAP1), mRNA. 7/21Length = 4422	vesicle associated protein
2355	25529	NM_033096	n,o	Rattus norvegicus Protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform (Ppm1b), mRNA. 7/21Length = 3257	Protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform
2355	25569	NM_033096	r	Rattus norvegicus Protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform (Ppm1b), mRNA. 7/21Length = 3257	Protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform
2355	19148	NM_033096	h,l	Rattus norvegicus Protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform (Ppm1b), mRNA. 7/21Length = 3257	Protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform
2356	25468	NM_033234	b,c,v	Rattus norvegicus Hemoglobin, beta (Hbb), mRNA. 12/21Length = 62	Hemoglobin, beta
2356	17829	NM_033234	c	Rattus norvegicus Hemoglobin, beta (Hbb), mRNA. 12/21Length = 62	Hemoglobin, beta
2356	17832	NM_033234	b,c,v	Rattus norvegicus Hemoglobin, beta (Hbb), mRNA. 12/21Length = 62	Hemoglobin, beta
2356	25469	NM_033234	b,c,v	Rattus norvegicus Hemoglobin, beta (Hbb), mRNA. 12/21Length = 62	
2357	2577	NM_033236	r	Rattus norvegicus Proteasome (prosome, macropain) 26S subunit, ATPase (Psmc2), mRNA. 8/21Length = 143	Proteasome (prosome, macropain) 26S subunit, ATPase
2358	23715	NM_033237	j,k,y,z,jj,kk	Rattus norvegicus galanin (Gal), mRNA. 11/22Length = 699	galanin
2359	12364	NM_033351	e,y,z,ee,ff	Rattus norvegicus Fc receptor, IgG, alpha chain transporter (Fcgrt), mRNA. 11/22Length = 1552	Fc fragment immunoglobulin G receptor
2359	12365	NM_033351	e	Rattus norvegicus Fc receptor, IgG, alpha chain transporter (Fcgrt), mRNA. 11/22Length = 1552	Fc fragment immunoglobulin G receptor

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2360	11714	NM_033352	kk	Rattus norvegicus ATP-binding cassette, sub-family D (ALD), member 2 (Abcd2), mRNA. 11/22Length = 5531	ESTs
2361	23895	NM_033485	aa	Rattus norvegicus PRKC, apoptosis, WT1, regulator (Pawr), mRNA. 11/22Length = 2122	Prostate apoptosis response protein 4
2362	24420	NM_033539	jj,kk,ll	Rattus norvegicus eukaryotic translation elongation factor 1alpha 2 (Eef1a2), mRNA. 11/22Length = 144	eukaryotic translation elongation factor 1 alpha 1
2362	24419	NM_033539	jj,kk	Rattus norvegicus eukaryotic translation elongation factor 1alpha 2 (Eef1a2), mRNA. 11/22Length = 144	eukaryotic translation elongation factor 1 alpha 1
2363	25072	NM_052807	j,k	Rattus norvegicus Insulin-like growth factor 1 receptor (Igf1r), mRNA. 1/21Length = 4696	Insulin-like growth factor 1 receptor
2364	15867	NM_053289	a,h,i,l,w,x	Rattus norvegicus Pancreatitis-associated protein 1 (Pap1), mRNA. 11/21Length = 781	ESTs, Weakly similar to R02D3.2.p [Caenorhabditis elegans] [C.elegans], Pancreatitis-associated protein 1
2365	1311	NM_053291	e	Rattus norvegicus Phosphoglycerate kinase 1 (Pkg), mRNA. 11/22Length = 1675	phosphoglycerate kinase 1
2366	1596	NM_053294	r	Rattus norvegicus Adenosine A2a-receptor (Adora2a), mRNA. 4/22Length = 2373	Adenosine A2a-receptor
2367	20235	NM_053302	cc,dd	Rattus norvegicus adrenomedullin receptor (Admr), mRNA. 11/22Length = 1197	ESTs, Weakly similar to dual-specificity phosphatase [Mus musculus] [M.musculus]
2368	15748	NM_053309	ii	Rattus norvegicus homer, neuronal immediate early gene, 2(Homer2), mRNA. 11/22Length = 1994	homer, neuronal immediate early gene, 2
2369	7207	NM_053326	hh	Rattus norvegicus enigma homolog (Enh), mRNA. 11/21Length = 1896	enigma homolog
2370	1063	NM_053328	e	Rattus norvegicus basic helix-loop-helix domain containing, class B2 (Bhlhb2), mRNA. 11/22Length = 2388	basic helix-loop-helix domain containing, class B2
2371	14927	NM_053330	e	Rattus norvegicus ribosomal protein L21 (Rpl21), mRNA. 11/22Length = 554	ribosomal protein L21
2371	14929	NM_053330	h,l	Rattus norvegicus ribosomal protein L21 (Rpl21), mRNA. 11/22Length = 554	ribosomal protein L21
2372	2674	NM_053333	gg	Rattus norvegicus resistin like alpha (Retnla), mRNA. 11/22Length = 54	resistin like alpha
2373	1609	NM_053338	j,p,q,y,z	Rattus norvegicus Ras-related associated with diabetes (Rrad), mRNA. 11/22Length = 1421	Ras-related associated with diabetes

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2374	18949	NM_053345	ii	Rattus norvegicus general transcription factor Ila, 2 (12kDsubunit) (Gtf2a2), mRNA. 11/21Length = 33	general transcription factor Ila, 2 (12kD subunit)
2375	9352	NM_053347	u,v	Rattus norvegicus nuclear distribution gene E homolog(Aspergillus) (Nude), mRNA. 11/22Length = 2153	nuclear distribution gene E homolog (Aspergillus)
2376	6154	NM_053356	f,g	Rattus norvegicus procollagen, type I, alpha 2 (Col1a2),mRNA. 11/22Length = 4474	procollagen, type I, alpha 2
2376	6155	NM_053356	g	Rattus norvegicus procollagen, type I, alpha 2 (Col1a2),mRNA. 11/22Length = 4474	procollagen, type I, alpha 2
2376	6156	NM_053356	g	Rattus norvegicus procollagen, type I, alpha 2 (Col1a2),mRNA. 11/22Length = 4474	procollagen, type I, alpha 2
2376	6157	NM_053356	f,g	Rattus norvegicus procollagen, type I, alpha 2 (Col1a2),mRNA. 11/22Length = 4474	procollagen, type I, alpha 2
2376	25184	NM_053356	f	Rattus norvegicus procollagen, type I, alpha 2 (Col1a2),mRNA. 11/22Length = 4474	
2377	19512	NM_053365	ii	Rattus norvegicus fatty acid binding protein 4 (Fabp4), mRNA. 11/22Length = 6	adipocyte lipid-binding protein
2378	622	NM_053369	a,j,k	Rattus norvegicus transcription factor 4 (Tcf4), mRNA. 1/22Length = 259	transcription factor 4
2378	623	NM_053369	r,hh	Rattus norvegicus transcription factor 4 (Tcf4), mRNA. 1/22Length = 259	transcription factor 4
2379	16017	NM_053401	o,aa	Rattus norvegicus nerve growth factor receptor (TNFRSF16) associated protein 1 (Ngfrap1), mRNA. 11/22Length = 519	brain expressed X-linked 3
2379	16018	NM_053401	b,c	Rattus norvegicus nerve growth factor receptor (TNFRSF16) associated protein 1 (Ngfrap1), mRNA. 11/22Length = 519	brain expressed X-linked 3
2380	14621	NM_053437	e,hh	Rattus norvegicus diacylglycerol O-acyltransferase 1 (Dgat1), mRNA. 11/22Length = 1751	diacylglycerol acyltransferase
2381	6712	NM_053448	cc,dd	Rattus norvegicus histone deacetylase 3 (Hdac3), mRNA. 11/22Length = 1799	histone deacetylase 3
2382	4622	NM_053463	l,m	Rattus norvegicus nucleobindin (Nucb), mRNA. 11/22Length = 233	nucleobindin

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2383	21866	NM_053472	u,v	Rattus norvegicus cytochrome c oxidase, subunit 4b (Cox4b), mRNA. 11/22Length = 74	cytochrome c oxidase, subunit IVb
2384	21498	NM_053474	gg	Rattus norvegicus spinophilin (LOC84686), mRNA. 11/21Length = 455	spinophilin
2385	15556	NM_053483	kk	Rattus norvegicus karyopherin (importin) alpha 2 (Kpna2), mRNA. 11/22Length = 1886	karyopherin (importin) alpha 2
2386	16394	NM_053485	h,l,w,x	Rattus norvegicus calcium binding protein A6 (calcyclin)(S1a6), mRNA. 11/21Length = 291	calcium binding protein A6 (calcyclin)
2387	14904	NM_053492	s,t	Rattus norvegicus transporter-like protein (Ct11), mRNA. 11/21Length = 2849	transporter-like protein
2388	16135	NM_053516	aa,bb	Rattus norvegicus unknown Glu-Pro dipeptide repeat protein(LOC85383), mRNA. 11/21Length = 1876	unknown Glu-Pro dipeptide repeat protein
2389	18826	NM_053523	bb	Rattus norvegicus homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (Herpud1), mRNA. 11/21Length = 1857	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
2390	14380	NM_053536	e,y,z	Rattus norvegicus Kruppel-like factor 15 (Klf15), mRNA. 11/22Length = 2458	Kruppel-like factor 15 (kidney)
2391	31	NM_053537	b	Rattus norvegicus solute carrier family 22 (organic anion transporter), member 7 (Slc22a7), mRNA. 1/22Length = 191	solute carrier family 22 (organic anion transporter), member 7
2392	15829	NM_053551	e,n,o,p,q,r,aa,bb	Rattus norvegicus pyruvate dehydrogenase kinase 4 (Pdk4), mRNA. 11/22Length = 1435	pyruvate dehydrogenase kinase, isoenzyme 4
2393	17298	NM_053553	cc,dd	Rattus norvegicus synaptogyrin 2 (Syngr2), mRNA. 11/21Length = 118	synaptogyrin 2
2394	11843	NM_053555	n,o,s	Rattus norvegicus vesicle-associated membrane protein 5 (Vamp5), mRNA. 11/21Length = 39	vesicle-associated membrane protein 5
2395	4327	NM_053563	a,n,o,y,z,jj,kk	Rattus norvegicus nuclear RNA helicase, DECD variant of DEADbox family (Ddx1), mRNA. 11/21Length = 1511	nuclear RNA helicase, DECD variant of DEAD box family
2396	15708	NM_053565	p,q,y,z	Rattus norvegicus cytokine inducible SH2-containing protein 3 (Cish3), mRNA. 11/21Length = 863	cytokine inducible SH2-containing protein 3
2397	21940	NM_053568	f	Rattus norvegicus phosphate cytidyltransferase 2, ethanolamine (Pcyt2), mRNA. 11/21Length = 1846	phosphate cytidyltransferase 2, ethanolamine



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2398	19252	NM_053576	a	Rattus norvegicus peroxiredoxin 5 (Prdx5), mRNA. 1/22Length = 1414	peroxiredoxin 5
2399	653	NM_053580	aa,bb	Rattus norvegicus fatty acid transport protein (Slc27a1), mRNA. 11/21Length = 398	fatty acid transport protein
2400	3049	NM_053582	j,k,t,kk	Rattus norvegicus glucocorticoid-inducible protein (gis5),mRNA. 11/21Length = 1869	glucocorticoid-inducible protein
2400	3050	NM_053582	j,k,t,kk	Rattus norvegicus glucocorticoid-inducible protein (gis5),mRNA. 11/21Length = 1869	glucocorticoid-inducible protein
2401	24875	NM_053583	ii,jj,kk	Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz(Roaz), mRNA. 11/21Length = 4665	Olf-1/EBF associated Zn finger protein Roaz
2402	21170	NM_053585	s,t	Rattus norvegicus MAP-kinase activating death domain (Madd),mRNA. 11/21Length = 5249	MAP-kinase activating death domain
2403	21445	NM_053587	a,e,y,z,ee,ff	Rattus norvegicus S1 calcium-binding protein A9(calgranulin B) (S1a9), mRNA. 11/21Length = 494	S100 calcium-binding protein A9 (calgranulin B)
2404	20896	NM_053592	h,i	Rattus norvegicus Deoxyuridinetriphosphatase (dUTPase) (Dut), mRNA. 5/22Length = 952	Deoxyuridinetriphosphatase (dUTPase)
2405	20902	NM_053593	r	Rattus norvegicus cyclin-dependent kinase 4 (Cdk4), mRNA.11/21Length = 1232	cyclin-dependent kinase 4
2406	21709	NM_053596	j,k,y,li	Rattus norvegicus Endothelin-converting enzyme 1 (Ece1), mRNA.5/22Length = 4469	Endothelin-converting enzyme 1
2407	2103	NM_053597	g	Rattus norvegicus ribosomal protein S27 (Rps27), mRNA. 11/22Length = 336	ribosomal protein S27
2408	11794	NM_053606	ii	Rattus norvegicus Matrix metalloproteinase 23 (Mmp23), mRNA. 11/21Length = 1444	Matrix metalloproteinase 23
2409	20243	NM_053615	aa,bb	Rattus norvegicus casein kinase 1, alpha 1 (Csnk1a1), mRNA. 11/21Length = 978	casein kinase 1, alpha 1
2410	13005	NM_053623	j,k,y,z	Rattus norvegicus fatty acid Coenzyme A ligase, long chain 4 (Facl4), mRNA. 11/22Length = 4862	fatty acid-Coenzyme A ligase, long chain 4
2411	1228	NM_053625	j,k	Rattus norvegicus G elongation factor (EF-G), mRNA. 11/21Length = 2619	G elongation factor
2412	15777	NM_053630	b,u,v	Rattus norvegicus potassium voltage-gated channel, subfamily H (eag-related), member 4 (Kcnh4), mRNA. 11/21Length = 3736	potassium voltage-gated channel, subfamily H (eag-related), member 4

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2413	857	NM_053633	y,z,ee,ff	Rattus norvegicus early growth response 2 (Egr2), mRNA. 11/21Length = 2976	early growth response 2
2414	18644	NM_053648	bb	Rattus norvegicus beta-carotene 15, 15-dioxygenase (Bcdo), mRNA. 11/22Length = 227	beta-carotene 15, 15'-dioxygenase
2415	1118	NM_053655	u	Rattus norvegicus dynamin 1-like (Dnml1), mRNA. 11/22Length = 3845	dynamin 1-like
2416	1316	NM_053656	s,t,ii	Rattus norvegicus purinergic receptor P2X, ligand-gated ion channel, 2 (P2rx2), mRNA. 11/22Length = 1831	purinergic receptor P2X, ligand-gated ion channel, 2
2417	3454	NM_053662	p,q	Rattus norvegicus cyclin L (Ccnl), mRNA. 11/21Length = 292	cyclin L
2417	3455	NM_053662	p,q,gg	Rattus norvegicus cyclin L (Ccnl), mRNA. 11/21Length = 292	cyclin L
2418	2063	NM_053682	e	Rattus norvegicus YME1 (S.cerevisiae)-like 1 (Yme1l1), mRNA. 11/21Length = 2727	YME1 (S.cerevisiae)-like 1
2419	16122	NM_053698	p,q,ee,ff	Rattus norvegicus Cbp/p3-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (Cited2), mRNA. 11/21Length = 1155	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
2419	16123	NM_053698	d,p,q,jj,kk	Rattus norvegicus Cbp/p3-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (Cited2), mRNA. 11/21Length = 1155	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
2420	6684	NM_053703	kk	Rattus norvegicus mitogen-activated protein kinase kinase 6 (Map2k6), mRNA. 11/22Length = 169	mitogen-activated protein kinase kinase 6
2421	13622	NM_053713	aa,bb,ll	Rattus norvegicus Kruppel-like factor 4 (gut) (Klf4), mRNA. 11/22Length = 2393	Kruppel-like factor 4 (gut)
2421	22411	NM_053713	d,t	Rattus norvegicus Kruppel-like factor 4 (gut) (Klf4), mRNA. 11/22Length = 2393	Kruppel-like factor 4 (gut)
2421	25379	NM_053713	t,ll	Rattus norvegicus Kruppel-like factor 4 (gut) (Klf4), mRNA. 11/22Length = 2393	Kruppel-like factor 4 (gut)
2422	15269	NM_053739	d,f,g	Rattus norvegicus beclin 1 (coiled-coil, myosin-like BCL2-interacting protein) (Becn1), mRNA. 11/21Length = 198	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)
2423	13369	NM_053742	n,o	Rattus norvegicus phosphatidylinositol transfer protein, beta (Pitpnb), mRNA. 11/22Length = 268	phosphatidylinositol transfer protein, beta
2424	10510	NM_053743	u,v	Rattus norvegicus cell division cycle 37 homolog (S. cerevisiae) (Cdc37), mRNA. 11/22Length = 164	CDC37 (cell division cycle 37, S. cerevisiae, homolog)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2425	18175	NM_053752	aa,bb	Rattus norvegicus succinate-CoA ligase, GDP-forming, alpha subunit (Succ1), mRNA. 11/21Length = 1684	succinate-CoA ligase, GDP-forming, alpha subunit
2426	7927	NM_053765	d	Rattus norvegicus UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase (Uae1), mRNA. 11/22Length = 258	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase
2427	15996	NM_053769	cc,dd	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 16 (Ptpn16), mRNA. 11/22Length = 198	protein tyrosine phosphatase, non-receptor type 16
2428	14015	NM_053770	hh	Rattus norvegicus Arg/Abl-interacting protein ArgBP2(Argbp2), mRNA. 11/21Length = 6331	Arg/Abl-interacting protein ArgBP2
2428	14017	NM_053770	hh	Rattus norvegicus Arg/Abl-interacting protein ArgBP2(Argbp2), mRNA. 11/21Length = 6331	Arg/Abl-interacting protein ArgBP2
2429	1016	NM_053772	r,gg	Rattus norvegicus protein kinase inhibitor, alpha (Pkia), mRNA. 11/21Length = 1183	protein kinase inhibitor, alpha
2430	9059	NM_053783	j,k,kk	Rattus norvegicus interferon gamma receptor (Ifngr), mRNA. 11/21Length = 186	interferon gamma receptor
2431	11606	NM_053795	gg	Rattus norvegicus kinase D-interacting substance of 22 kDa (Kidins22), mRNA. 3/22Length = 714	kinase D-interacting substance of 220 kDa
2432	25594	NM_053799	jj,kk,ll	Rattus norvegicus aspartyl-tRNA synthetase (Dars), mRNA. 11/21Length = 2143	aspartyl-tRNA synthetase
2433	15615	NM_053800	h,l	Rattus norvegicus thioredoxin (Txn), mRNA. 11/22Length = 33	thioredoxin
2434	25262	NM_053814	b,u,v,cc,dd	Rattus norvegicus Rho interacting protein 3 (Rhoip3), mRNA. 11/21Length = 3286	Rho interacting protein 3
2435	15002	NM_053819	a,l,k,n,o,x,z,hh,kk	Rattus norvegicus tissue inhibitor of metalloproteinase 1 (Timp1), mRNA. 11/21Length = 74	tissue inhibitor of metalloproteinase 1
2435	15003	NM_053819	a,l,k,n,o,x,z,hh,kk	Rattus norvegicus tissue inhibitor of metalloproteinase 1 (Timp1), mRNA. 11/21Length = 74	tissue inhibitor of metalloproteinase 1
2436	20421	NM_053821	f,ii	Rattus norvegicus v-ral simian leukemia viral oncogene homolog B (ras related) (Ralb), mRNA. 11/21Length = 274	v-ral simian leukemia viral oncogene homolog B (ras related)
2437	16173	NM_053822	e,y,z,ee,ff	Rattus norvegicus S1 calcium-binding protein A8 (calgranulin A) (S1a8), mRNA. 11/21Length = 361	S100 calcium-binding protein A8 (calgranulin A)

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2438	17154	NM_053835	b,gg	Rattus norvegicus clathrin, light polypeptide (Lcb) (Cltb), mRNA. 11/22Length = 982	clathrin, light polypeptide (Lcb)
2438	17155	NM_053835	g	Rattus norvegicus clathrin, light polypeptide (Lcb) (Cltb), mRNA. 11/22Length = 982	clathrin, light polypeptide (Lcb)
2438	18065	NM_053835	c	Rattus norvegicus clathrin, light polypeptide (Lcb) (Cltb), mRNA. 11/22Length = 982	clathrin, light polypeptide (Lcb)
2439	16099	NM_053837	f,r,cc,dd	Rattus norvegicus adaptor-related protein complex 2, mu 1 subunit (Ap2m1), mRNA. 11/21Length = 1816	adaptor-related protein complex 2, mu 1 subunit
2440	20868	NM_053843	kk	Rattus norvegicus Fc receptor, IgG, low affinity III (Fcgr3), mRNA. 11/22Length = 1318	Fc receptor, IgG, low affinity III
2440	20869	NM_053843	w,x,kk	Rattus norvegicus Fc receptor, IgG, low affinity III (Fcgr3), mRNA. 11/22Length = 1318	Fc receptor, IgG, low affinity III
2441	1780	NM_053846	u,v	Rattus norvegicus neuexin 2 (Nrxn2), mRNA. 11/21Length = 6436	neuexin 2
2442	1011	NM_053851	e	Rattus norvegicus calcium channel, voltage-dependent, beta 2subunit (Cacnb2), mRNA. 11/22Length = 3927	calcium channel, voltage-dependent, beta 2 subunit
2443	16361	NM_053853	cc,dd	Rattus norvegicus N-acetyltransferase 1 (arylamine N-acetyltransferase) (Nat1), mRNA. 11/22Length = 2533	N-acetyltransferase 1 (arylamine N-acetyltransferase)
2444	1570	NM_053857	s,t	Rattus norvegicus eukaryotic translation initiation factor4E binding protein 1 (Eif4ebp1), mRNA. 11/22Length = 843	eukaryotic translation initiation factor 4E binding protein 1
2444	1571	NM_053857	e,t,kk	Rattus norvegicus eukaryotic translation initiation factor4E binding protein 1 (Eif4ebp1), mRNA. 11/22Length = 843	eukaryotic translation initiation factor 4E binding protein 1
2445	18357	NM_053864	n,o	Rattus norvegicus valosin-containing protein (Vcp), mRNA. 11/22Length = 287	valosin-containing protein
2446	11405	NM_053866	f	Rattus norvegicus phospholipase A2, activating protein (Pla2), mRNA. 11/21Length = 2451	phospholipase A2, activating protein
2447	1352	NM_053880	aa	Rattus norvegicus dynein, cytoplasmic, intermediate polypeptide 2 (Dnci2), mRNA. 11/21Length = 2538	dynein, cytoplasmic, intermediate polypeptide 2
2448	20939	NM_053884	gg	Rattus norvegicus ATPase, vacuolar, 14 kD (Atp6s14), mRNA. 11/21Length = 667	ATPase, vacuolar, 14 kD

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2449	385	NM_053885	b,o,u,v,ee,ff,kk	Rattus norvegicus arginine-glutamic acid dipeptide (RE) repeats(Rere), mRNA. 11/21Length = 6659	arginine-glutamic acid dipeptide (RE) repeats
2450	753	NM_053897	ee,ff,gg	Rattus norvegicus Proteinase-activated receptor-2, G protein-coupled receptor 11 (F2rl1), mRNA. 5/22Length = 1428	Proteinase-activated receptor-2, G protein-coupled receptor 11
2451	15706	NM_053921	ll	Rattus norvegicus peroxisomal biogenesis factor 12 (Pex12), mRNA. 11/21Length = 2347	peroxisomal biogenesis factor 12
2452	1426	NM_053950	aa	Rattus norvegicus eukaryotic translation initiation factor 2B (Eif2b), mRNA. 11/21Length = 1634	eukaryotic translation initiation factor 2B
2453	531	NM_053951	gg	Rattus norvegicus MCF.2 cell line derived transforming sequence-like (Mcf2l), mRNA. 11/21Length = 4354	MCF.2 cell line derived transforming sequence-like
2454	16552	NM_053961	h,l,n,o	Rattus norvegicus endoplasmic reticulum protein 29 (Erp29), mRNA. 11/21Length = 4529	endoplasmic reticulum protein 29
2454	16553	NM_053961	h,l	Rattus norvegicus endoplasmic reticulum protein 29 (Erp29), mRNA. 11/21Length = 4529	endoplasmic reticulum protein 29
2455	16654	NM_053963	n,o	Rattus norvegicus matrix metalloproteinase 12 (Mmp12), mRNA. 11/21Length = 1632	matrix metalloproteinase 12
2456	16546	NM_053965	hh	Rattus norvegicus solute carrier family 25(carnitine/acylcarnitine translocase), member 2 (Slc25a2), mRNA.11/21Length = 1231	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
2456	16547	NM_053965	hh	Rattus norvegicus solute carrier family 25(carnitine/acylcarnitine translocase), member 2 (Slc25a2), mRNA.11/21Length = 1231	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
2457	6357	NM_053969	d	Rattus norvegicus G protein pathway suppressor 1 (Gps1), mRNA.11/21Length = 1794	G protein pathway suppressor 1
2458	15135	NM_053971	h,l,n,o,w,x	Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 11/21Length = 963	ribosomal protein L6
2458	15136	NM_053971	h,l,w,ii	Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 11/21Length = 963	ribosomal protein L6
2458	22183	NM_053971	h,l	Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. 11/21Length = 963	EST
2459	15343	NM_053973	aa	Rattus norvegicus Ras-related GTP-binding protein ragA (Raga),mRNA. 11/21Length = 161	Ras-related GTP-binding protein ragA

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2460	18798	NM_053978	h,i,n,o	Rattus norvegicus RAB28, member RAS oncogene family (Rab28), mRNA. 11/21Length = 1483	RAB28, member RAS oncogene family
2461	15468	NM_053982	j,w,x,jj,kk	Rattus norvegicus ribosomal protein S15a (Rps15a), mRNA. 11/21Length = 449	ribosomal protein S15a
2462	15642	NM_053985	d	Rattus norvegicus H3 histone, family 3B (H3f3b), mRNA. 11/21Length = 117	H3 histone, family 3B
2462	15645	NM_053985	d	Rattus norvegicus H3 histone, family 3B (H3f3b), mRNA. 11/21Length = 117	H3 histone, family 3B
2463	17653	NM_053986	cc,dd	Rattus norvegicus myosin Ib (Myo1b), mRNA. 11/22Length = 367	myosin IB
2464	18025	NM_053989	w,x	Rattus norvegicus progesterone induced protein (dd5), mRNA. 11/21Length = 318	progesterone induced protein
2465	17739	NM_053995	g	Rattus norvegicus 3-hydroxybutyrate dehydrogenase (heart, mitochondrial) (Bdh), mRNA. 11/21Length = 142	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)
2466	16962	NM_053999	u,v	Rattus norvegicus protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (Ppp2r2a), mRNA. 11/21Length = 2142	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
2467	25249	NM_054001	n,o	Rattus norvegicus CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (Cd36l2), mRNA. 11/21Length = 1938	
2468	16566	NM_054004	hh	Rattus norvegicus TBP-interacting protein 12A (Tip12A), mRNA. 11/21Length = 4383	TBP-interacting protein 120A
2469	1108	NM_054005	b,i,m	Rattus norvegicus integral membrane-associated protein 1 (Itmap1), mRNA. 11/21Length = 2282	integral membrane-associated protein 1
2470	17431	NM_054006	cc,dd	Rattus norvegicus unr protein (unr), mRNA. 11/21Length = 3755	unr protein
2471	17326	NM_054008	s,t	Rattus norvegicus Rgc32 protein (Rgc32), mRNA. 11/21Length = 889	Rgc32 protein
2471	17330	NM_054008	aa,bb	Rattus norvegicus Rgc32 protein (Rgc32), mRNA. 11/21Length = 889	Rgc32 protein
2472	23250	NM_057097	f,g	Rattus norvegicus vesicle-associated membrane protein 3 (Vamp3), mRNA. 11/22Length = 1742	vesicle-associated membrane protein 3
2473	25290	NM_057100	d,u,v	Rattus norvegicus growth arrest specific 6 (Gas6), mRNA. 11/22Length = 2573	growth arrest specific 6

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2474	17709	NM_057101	u,v	Rattus norvegicus Cytochrome P45, subfamily XXI (steroid 21-hydroxylase) (Cyp21), mRNA. 1/22Length = 1964	Tenascin X
2475	19658	NM_057103	gg	Rattus norvegicus A kinase (PRKA) anchor protein (gravin) 12(Akap12), mRNA. 11/22Length = 5236	A kinase (PRKA) anchor protein (gravin) 12
2476	9528	NM_057104	r	Rattus norvegicus ectonucleotide pyrophosphatase/phosphodiesterase 2 (Enpp2), mRNA. 11/22Length = 3216	ectonucleotide pyrophosphatase/phosphodiesterase 2
2477	15125	NM_057105	jj,kk,ll	Rattus norvegicus UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/22Length = 1593	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A7
2478	15391	NM_057114	d	Rattus norvegicus peroxiredoxin 1 (Prdx1), mRNA. 11/21Length = 882	peroxiredoxin 1
2479	23307	NM_057119	e	Rattus norvegicus splicing factor, arginine/serine-rich(transformer 2 Drosophila homolog) 1 (Sfrs1), mRNA. 11/21Length = 1978	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10
2479	23310	NM_057119	e,s,t	Rattus norvegicus splicing factor, arginine/serine-rich(transformer 2 Drosophila homolog) 1 (Sfrs1), mRNA. 11/21Length = 1978	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10
2480	727	NM_057123	s,t	Rattus norvegicus protease (prosome, macropain) 26S subunit, ATPase 1 (Psmc1), mRNA. 11/21Length = 1556	protease (prosome, macropain) 26S subunit, ATPase 1
2481	919	NM_057125	l,m	Rattus norvegicus peroxisomal biogenesis factor 6 (Pex6), mRNA. 11/21Length = 3169	peroxisomal biogenesis factor 6
2482	2413	NM_057141	b,g,n,o,u,v	Rattus norvegicus heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563	heterogeneous nuclear ribonucleoprotein K
2482	2416	NM_057141	t	Rattus norvegicus heterogeneous nuclear ribonucleoprotein K (Hnrpk), mRNA. 11/22Length = 2563	heterogeneous nuclear ribonucleoprotein K
2483	1892	NM_057144	a,o,x,ee,ff,kk	Rattus norvegicus cysteine-rich protein 3 (Csrp3), mRNA. 11/22Length = 853	cysteine-rich protein 3
2484	19481	NM_057153	a,y,z,ee,ff	Rattus norvegicus oxidation resistance 1 (Oxr1), mRNA. 11/21Length = 1896	oxidation resistance 1
2485	15460	NM_057191	d,ee,ff	Rattus norvegicus sarcomeric muscle protein (Sarcosin),mRNA. 11/21Length = 2316	sarcomeric muscle protein

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2485	15461	NM_057191	ee,ff	Rattus norvegicus sarcomeric muscle protein (Sarcosin), mRNA. 11/21Length = 2316	sarcomeric muscle protein
2486	15408	NM_057197	f,g,l,m	Rattus norvegicus 2,4-dienoyl CoA reductase 1, mitochondrial (Decr1), mRNA. 11/22Length = 119	2,4-dienoyl CoA reductase 1, mitochondrial
2486	15409	NM_057197	f,g	Rattus norvegicus 2,4-dienoyl CoA reductase 1, mitochondrial (Decr1), mRNA. 11/22Length = 119	2,4-dienoyl CoA reductase 1, mitochondrial
2487	18122	NM_057208	h,l	Rattus norvegicus tropomyosin 3, gamma (Tpm3), mRNA. 11/21Length = 111	tropomyosin 3, gamma
2488	1743	NM_057210	hh	Rattus norvegicus synaptic vesicle glycoprotein 2 a (Sv2a), mRNA. 11/21Length = 3844	synaptic vesicle glycoprotein 2 a
2489	8641	NM_057211	bb	Rattus norvegicus Kruppel-like factor 9 (Klf9), mRNA. 11/22Length = 2721	Kruppel-like factor 9
2490	11632	NM_057212	b	Rattus norvegicus brain specific binding protein (LOC117582), mRNA. 11/22Length = 999	brain specific binding protein
2491	15707	NM_058208	d	Rattus norvegicus cytokine inducible SH2-containing protein 2 (Cish2), mRNA. 11/22Length = 918	cytokine inducible SH2-containing protein 2
2492	10498	NM_078617	c,g,w,x	Rattus norvegicus ribosomal protein S23 (Rps23), mRNA. 11/22Length = 432	ribosomal protein S23
2493	8820	NM_080399	j,k,ee,ff,jj,kk	Rattus norvegicus Smhs1 protein (Smhs1), mRNA. 12/21Length = 117	Smhs1 protein
2494	2541	NM_080479	aa,bb	Rattus norvegicus melanoma antigen, family D, 2 (Maged2), mRNA. 12/21Length = 1993	melanoma antigen, family D, 2
2495	17958	NM_080583	gg	Rattus norvegicus adaptor-related protein complex 2, beta 1 subunit (Ap2b1), mRNA. 11/22Length = 5413	adaptor-related protein complex 2, beta 1 subunit
2495	17960	NM_080583	r	Rattus norvegicus adaptor-related protein complex 2, beta 1 subunit (Ap2b1), mRNA. 11/22Length = 5413	adaptor-related protein complex 2, beta 1 subunit
2496	506	NM_080586	ii	Rattus norvegicus gamma-aminobutyric acid (GABA) A receptor, gamma 1 (Gabrg1), mRNA. 1/22Length = 1739	gamma-aminobutyric acid (GABA) A receptor, gamma 1
2497	17662	NM_080697	cc,dd	Rattus norvegicus dynein light chain-2 (Dlc2), mRNA. 1/22Length = 51	dynein light chain-2
2498	23551	NM_080698	ii	Rattus norvegicus fibromodulin (Fmod), mRNA. 11/22Length = 296	fibromodulin



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2499	363	NM_080780	d,e,p,q,ee,ff	Rattus norvegicus purinergic receptor P2X, ligand-gated ion channel, 5 (P2rx5), mRNA. 1/22Length = 1558	purinergic receptor P2X, ligand-gated ion channel, 5
2500	23033	NM_080888	r	Rattus norvegicus BCL2/adenovirus E1B 19 kDa-interacting protein 3-like (Bnip3l), mRNA. 1/22Length = 3219	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like
2501	9952	NM_080902	cc,dd	Rattus norvegicus hypoxia induced gene 1 (Hig1), mRNA. 1/22Length = 355	hypoxia induced gene 1
2502	4739	NM_130400	aa,bb	Rattus norvegicus Dihydrofolate reductase 1 (active) (Dhfr1), mRNA. 1/22Length = 761	Dihydrofolate reductase 1 (active)
2503	9633	NM_130403	jj,kk	Rattus norvegicus protein phosphatase 1, regulatory(inhibitor) subunit 14a (Ppp1r14a), mRNA. 1/22Length = 559	protein phosphatase 1, regulatory (inhibitor) subunit 14a
2504	21695	NM_130411	c	Rattus norvegicus coronin, actin binding protein 1A (Coro1a),mRNA. 1/22Length = 1386	coronin, actin binding protein 1A
2505	11709	NM_130431	s	Rattus norvegicus heat shock 27kD protein 2 (Hspb2), mRNA. 11/22Length = 549	heat shock 27kD protein 2
2506	14959	NM_130734	w,x	Rattus norvegicus guanine nucleotide binding protein, betapolypeptide 2-like 1 (Gnb2l1), mRNA. 11/22Length = 189	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
2507	1809	NM_130741	l,k	Rattus norvegicus lipocalin 2 (Lcn2), mRNA. 11/22Length = 876	lipocalin 2
2508	1502	NM_130746	aa	Rattus norvegicus solute carrier family 5, member 6 (Slc5a6),mRNA. 11/22Length = 391	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
2508	1503	NM_130746	d	Rattus norvegicus solute carrier family 5, member 6 (Slc5a6),mRNA. 11/22Length = 391	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
2509	20738	NM_131907	c	Rattus norvegicus ATPase, Ca <sup>++</sup> -sequestering (Atp2c1), mRNA.11/22Length = 4645	ATPase, Ca <sup>++</sup> -sequestering
2510	17564	NM_133283	hh	Rattus norvegicus mitogen activated protein kinase kinase 2(Map2k2), mRNA. 11/22Length = 1376	mitogen activated protein kinase kinase 2
2511	25730	NM_133290	j,k,p,q	Rattus norvegicus zinc finger protein 36 (Zfp36), mRNA. 11/22Length = 963	zinc finger protein 36
2512	20879	NM_133295	hh	Rattus norvegicus carboxylesterase 3 (Ces3), mRNA. 11/22Length = 1935	carboxylesterase 3

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2513	19456	NM_133298	h,l,w,x	Rattus norvegicus glycoprotein (transmembrane) nmb (Gpnmb), mRNA. 2/22Length = 232	glycoprotein (transmembrane) nmb
2513	4048	NM_133298	h,l,n,o,w,x	Rattus norvegicus glycoprotein (transmembrane) nmb (Gpnmb), mRNA. 2/22Length = 232	glycoprotein (transmembrane) nmb
2513	4049	NM_133298	c,h,l,n,o,w,x	Rattus norvegicus glycoprotein (transmembrane) nmb (Gpnmb), mRNA. 2/22Length = 232	glycoprotein (transmembrane) nmb
2514	1061	NM_133303	p,q,hh	Rattus norvegicus basic helix-loop-helix domain containing, class B3 (Bhlhb3), mRNA. 11/22Length = 311	basic helix-loop-helix domain containing, class B, 3
2515	4318	NM_133306	p,q	Rattus norvegicus oxidised low density lipoprotein (lectin-like) receptor 1 (Olr1), mRNA. 11/22Length = 375	oxidised low density lipoprotein (lectin-like) receptor 1
2516	657	NM_133380	j,k,y,z	Rattus norvegicus Interleukin 4 receptor (Il4r), mRNA. 3/22Length = 3576	Interleukin 4 receptor
2517	7700	NM_133386	ee,ff	Rattus norvegicus sphingosine kinase 1 (Sphk1), mRNA. 11/22Length = 2648	sphingosine kinase 1
2518	16713	NM_133409	b	Rattus norvegicus integrin-linked kinase (Ilk), mRNA. 3/22Length = 1359	integrin-linked kinase
2519	19326	NM_133419	u,v,jj,kk	Rattus norvegicus dyskeratosis congenita 1, dyskerin (Dkc1), mRNA. 3/22Length = 183	dyskeratosis congenita 1, dyskerin
2520	10660	NM_133423	e,cc,dd	Rattus norvegicus splicing factor YT521-B (YT521), mRNA. 3/22Length = 2968	splicing factor YT521-B
2521	24775	NM_133511	c	Rattus norvegicus adenylate cyclase activating polypeptide 1 receptor 1 (Adcyap1r1), mRNA. 11/22Length = 2681	adenylate cyclase activating polypeptide 1 receptor 1
2522	25543	NM_133524	s	Rattus norvegicus transcription factor E2a (Tcf2a), mRNA. 3/22Length = 216	
2523	20890	NM_133526	ii	Rattus norvegicus transmembrane 4 superfamily member 3 (Tm4sf3), mRNA. 3/22Length = 1182	transmembrane 4 superfamily member 3
2524	2788	NM_133528	s,t	Rattus norvegicus preimplantation protein 3 (Prei3), mRNA. 3/22Length = 2513	preimplantation protein 3
2525	1791	NM_133541	li	Rattus norvegicus general transcription factor III C 1 (Gtf3c1), mRNA. 3/22Length = 6878	general transcription factor III C 1
2526	1824	NM_133545	j,k,r	Rattus norvegicus protein tyrosine phosphatase 2E (Ptp2E), mRNA. 3/22Length = 5543	protein tyrosine phosphatase 2E

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2527	11483	NM_133546	j,k,p,q,kk	Rattus norvegicus myeloid differentiation primary response gene 116 (Myd116), mRNA. 3/22Length = 2225	myeloid differentiation primary response gene 116
2527	18043	NM_133546	s,t,ll	Rattus norvegicus myeloid differentiation primary response gene 116 (Myd116), mRNA. 3/22Length = 2225	myeloid differentiation primary response gene 116
2528	244	NM_133551	a,j,k,y,z,ee,ff,kk	Rattus norvegicus phospholipase A2, group IVA (cytosolic, calcium-dependent) (Pla2g4a), mRNA. 1/22Length = 2858	EST, Weakly similar to FGD1_MOUSE Putative Rho/Rac guanine nucleotide exchange factor (Rho/Rac GEF) (Faclogenic dysplasia protein homolog) [M.musculus], phospholipase A2, group IVA (cytosolic, calcium-dependent)
2529	25369	NM_133559	l,m	Rattus norvegicus proprotein convertase subtilisin/kexin type 4 (Pcsk4), mRNA. 11/22Length = 2458	proprotein convertase subtilisin/kexin type 4
2530	1827	NM_133572	r,u,v	Rattus norvegicus cell division cycle 25B (Cdc25b), mRNA. 3/22Length = 284	cell division cycle 25B
2530	1830	NM_133572	v	Rattus norvegicus cell division cycle 25B (Cdc25b), mRNA. 3/22Length = 284	cell division cycle 25B
2530	1831	NM_133572	v	Rattus norvegicus cell division cycle 25B (Cdc25b), mRNA. 3/22Length = 284	cell division cycle 25B
2531	24609	NM_133585	cc,dd	Rattus norvegicus RN protein (LOC171116), mRNA. 3/22Length = 1619	RN protein
2532	1271	NM_133593	a,ee,ff,jj,kk	Rattus norvegicus adaptor-related protein complex AP-3, mu 1 subunit (Ap3m1), mRNA. 4/22Length = 2146	adaptor-related protein complex AP-3, mu 1 subunit
2533	1728	NM_133618	w,x	Rattus norvegicus hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (Hadhb), mRNA. 3/22Length = 1928	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
2534	14995	NM_133624	d	Rattus norvegicus guanylate binding protein 2, interferon-inducible (Gbp2), mRNA. 3/22Length = 2396	guanylate binding protein 2, interferon-inducible
2535	1463	NM_134334	u,v,gg	Rattus norvegicus cathepsin D (Ctsd), mRNA. 11/22Length = 1934	cathepsin D
2536	16456	NM_134346	ii	Rattus norvegicus RAP1B, member of RAS oncogene family (Rap1b), mRNA. 3/22Length = 1874	RAP1B, member of RAS oncogene family
2537	517	NM_134350	s	Rattus norvegicus myxovirus (influenza virus) resistance 3 (Mx3), mRNA. 3/22Length = 2443	myxovirus (influenza virus) resistance 3

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2538	17337	NM_134351	j,k	Rattus norvegicus methionine adenosyltransferase II, alpha (Mat2a), mRNA. 3/22Length = 1337	ESTs
2539	606	NM_134352	a,y,z	Rattus norvegicus Plasminogen activator, urokinase receptor (Plaur), mRNA. 5/22Length = 1277	Plasminogen activator, urokinase receptor
2540	19840	NM_134353	ll	Rattus norvegicus poly(A) binding protein, cytoplasmic 1(Pabpc1), mRNA. 3/22Length = 219	poly(A) binding protein, cytoplasmic 1
2541	8692	NM_134387	hh	Rattus norvegicus diacetyl/L-xylulose reductase (glb), mRNA. 3/22Length = 879	diacetyl/L-xylulose reductase
2542	1530	NM_134397	a,e,jj,kk	Rattus norvegicus LL5 protein (LI5), mRNA. 3/22Length = 3765	LL5 protein
2543	7164	NM_134406	jj,kk	Rattus norvegicus cytosolic sorting protein PACS-1 (Pacs1), mRNA. 3/22Length = 4198	cytosolic sorting protein PACS-1
2544	25237	NM_134452	r	Rattus norvegicus collagen, type V, alpha 1 (Col5a1), mRNA. 11/22Length = 5551	collagen, type V, alpha 1
2545	19077	NM_134455	aa,bb	Rattus norvegicus chemokine (C-X3-C motif) ligand 1 (Cx3cl1),mRNA. 1/22Length = 344	small inducible cytokine subfamily D, 1
2546	19894	NM_138518	t,ll	Rattus norvegicus late gestation lung protein 1 (Lgl1), mRNA. 4/22Length = 352	late gestation lung protein 1
2547	4422	NM_138531	gg	Rattus norvegicus associated molecule with the SH3 domain of STAM (Amsh), mRNA. 11/22Length = 1544	associated molecule with the SH3 domain of STAM
2548	5283	NM_138535	gg	Rattus norvegicus glutamate receptor interacting protein 2 (Grip2), mRNA. 4/22Length = 5433	glutamate receptor interacting protein 2
2549	25479	NM_138549	jj,kk	Rattus norvegicus synaptic glycoprotein SC2 (SC2), mRNA. 4/22Length = 1178	synaptic glycoprotein SC2
2550	15189	NM_138826	j,k,y,z,ee,ff,kk	Rattus norvegicus Metallothionein (Mt1a), mRNA. 11/22Length = 389	Metallothionein
2550	15190	NM_138826	j,k,y,z,ii	Rattus norvegicus Metallothionein (Mt1a), mRNA. 11/22Length = 389	Metallothionein
2551	16248	NM_138827	y,z	Rattus norvegicus solute carrier family 2,member 1 (Slc2a1),mRNA. 1/22Length = 2571	Solute carrier family 2 a 1 (facilitated glucose transporter) brain
2551	16249	NM_138827	j,k	Rattus norvegicus solute carrier family 2,member 1 (Slc2a1),mRNA. 1/22Length = 2571	Solute carrier family 2 a 1 (facilitated glucose transporter) brain

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2552	16400	NM_138828	cc,dd	Rattus norvegicus apolipoprotein E (Apoe), mRNA. 11/22Length = 936	Apolipoprotein E,
2552	16401	NM_138828	gg	Rattus norvegicus apolipoprotein E (Apoe), mRNA. 11/22Length = 936	
2553	23166	NM_138839	y,z,ee,ff,kk	Rattus norvegicus vacuole Membrane Protein 1 (Vmp1), mRNA. 11/22Length = 183	Vacuole Membrane Protein 1
2554	9796	NM_138847	j,k	Rattus norvegicus Saccharomyces cerevisiae Nip7p homolog(pEachy), mRNA. 4/22Length = 1175	Saccharomyces cerevisiae Nip7p homolog
2555	8468	NM_138861	b	Rattus norvegicus prolactin-like protein K (Prpk), mRNA. 11/22Length = 865	prolactin-like protein K
2556	17530	NM_138877	n,o,ii	Rattus norvegicus Diaphorase (NADH) (cytochrome b-5 reductase)(Dia1), mRNA. 4/22Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
2556	17532	NM_138877	j,k	Rattus norvegicus Diaphorase (NADH) (cytochrome b-5 reductase)(Dia1), mRNA. 4/22Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
2556	25039	NM_138877	ee,ff	Rattus norvegicus Diaphorase (NADH) (cytochrome b-5 reductase)(Dia1), mRNA. 4/22Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
2557	4594	NM_138881	c	Rattus norvegicus Best5 protein (Best5), mRNA. 4/22Length = 3628	Best5 protein
2558	945	NM_138882	j,k,s,t	Rattus norvegicus phosphatidylserine-specific phospholipase A1 (Pspla1), mRNA. 11/22Length = 1743	phosphatidylserine-specific phospholipase A1
2559	7395	NM_138883	r	Rattus norvegicus ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (Atp5o), mRNA. 4/22Length = 77	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
2560	3015	NM_138895	aa,bb	Rattus norvegicus polyubiquitin (Loc192255), mRNA. 4/22Length = 1115	polyubiquitin
2561	1168	NM_138898	e,n	Rattus norvegicus phospholipase B (Loc192259), mRNA. 4/22Length = 459	phospholipase B
2562	18867	NM_138900	b,c	Rattus norvegicus complement component 1, s subcomponent (C1s), mRNA. 11/22Length = 298	complement component 1, s subcomponent
2563	11840	NM_138911	e	Rattus norvegicus stress-induced-phosphoprotein 1 (Hsp7/Hsp9-organizing protein) (Stip1), mRNA. 4/22Length = 1632	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)
2564	15380	NM_139083	u,v,cc,dd	Rattus norvegicus ribosomal protein L41 (Rpl41), mRNA. 11/22Length = 357	ribosomal protein L41

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2565	734	NM_139094	gg	Rattus norvegicus CTD-binding SR-like protein rA8 (LOC245926), mRNA. 5/22Length = 4794	CTD-binding SR-like protein rA8
2566	17203	NM_139099	g,hh	Rattus norvegicus ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit (Atp5e), mRNA. 5/22Length = 44	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
2566	17204	NM_139099	g	Rattus norvegicus ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit (Atp5e), mRNA. 5/22Length = 44	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
2567	17854	NM_139103	ii	Rattus norvegicus CD48 antigen (Cd48), mRNA. 5/22Length = 1422	CD48 antigen
2568	17868	NM_139104	r,s,t	Rattus norvegicus Estrogen-regulated protein CBL2, 2.4kD (LOC245963), mRNA. 5/22Length = 1888	ESTs, Weakly similar to T09065 hypothetical protein - mouse [M.musculus], Estrogen-regulated protein CBL20, 20.4kD
2569	18108	NM_139105	a,n,o,ll	Rattus norvegicus ribonuclease/angiogenin inhibitor (Rnh1), mRNA. 11/22Length = 1664	ribonuclease/angiogenin inhibitor
2570	14463	NM_139110	ii	Rattus norvegicus G protein-coupled hepta-helical receptor Ig-Hepta (Ig-Hepta), mRNA. 5/22Length = 4951	G protein-coupled hepta-helical receptor Ig-Hepta
2571	22595	NM_139253	cc,dd	Rattus norvegicus stem cell derived neuronal survival protein precursor (Sdnf), mRNA. 5/22Length = 1771	stem cell derived neuronal survival protein precursor
2572	1803	NM_139256	c	Rattus norvegicus mannosidase, alpha, class 2C, member 1(Man2c1), mRNA. 5/22Length = 336	mannosidase, alpha, class 2C, member 1
2573	9775	NM_139334	c	Rattus norvegicus brain-enriched SH3-domain protein Besh3 (Besh3), mRNA. 11/22Length = 2362	brain-enriched SH3-domain protein Besh3
2574	12450	NM_139337	c,hh	Rattus norvegicus LRP16 protein (Lrp16), mRNA. 11/22Length = 13	Rattus norvegicus LRP16-like protein mRNA, complete cds
2575	21818	NM_139342	bb	Rattus norvegicus homocysteine respondent protein HCYP2 (Hcyp2), mRNA. 11/22Length = 215	Rattus norvegicus homocysteine respondent protein HCYP2 mRNA, complete cds
2576	12804	NM_144740	l,m	Rattus norvegicus Rho GTPase activating protein 4 (Arhgap4), mRNA. 11/22Length = 325	ESTs, Moderately similar to RHG4_HUMAN Rho-GTPase-activating protein 4 (Rho-GAP hematopoietic protein C1) (P115) [H.sapiens]
2577	13712	NM_144744	ii	Rattus norvegicus adipocyte complement related protein of 3kDa (Acrp3), mRNA. 11/22Length = 767	ESTs, Weakly similar to 1917150A collagen:SUBUNIT=alpha1:ISOTYPE=VIII [Rattus norvegicus] [R.norvegicus]
2578	23756	NM_145084	gg	Rattus norvegicus hypothetical protein RMT-7 (Rmt7), mRNA. 11/22Length = 1855	Rattus norvegicus hypothetical protein RMT-7 mRNA, complete cds

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2579	15761	NM_145091	cc,dd,jj,kk	Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme2 (Pdp2), mRNA. 11/22Length = 175	Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 2 mRNA, complete cds
2580	1948	NM_145092	b,l,m	Rattus norvegicus lamina-associated polypeptide 1C (Lap1c), mRNA. 11/22Length = 231	Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds
2581	6731	NM_145096	hh	Rattus norvegicus zinc finger, DHHC domain containing 2(Zdhc2), mRNA. 11/22Length = 1487	Rattus norvegicus small rec (srec) mRNA, complete cds
2582	6988	NM_145677	j,k	Rattus norvegicus peroxisomal Ca-dependent solute carrier-like protein (Pcscl), mRNA. 11/22Length = 315	ESTs
2583	305	NM_145773	u,v	Rattus norvegicus Max dimerization protein 3 (Mad3), mRNA. 11/22Length = 989	Rattus norvegicus Myx mRNA, complete cds
2584	15640	NM_145775	h,l,j,k,r	Rattus norvegicus nuclear receptor subfamily 1, group D, member 1 (Nr1d1), mRNA. 11/22Length = 2297	Rat Rev-ErbA-alpha protein mRNA, complete cds
2584	15641	NM_145775	h,l	Rattus norvegicus nuclear receptor subfamily 1, group D, member 1 (Nr1d1), mRNA. 11/22Length = 2297	Rat Rev-ErbA-alpha protein mRNA, complete cds
2585	22972	NM_145778	e	Rattus norvegicus tubulin, gamma 1 (Tubg1), mRNA. 11/22Length = 142	Rattus norvegicus mRNA for tubulin, complete cds
2586	20106	NM_145784	ii	Rattus norvegicus G protein-coupled receptor 37-like 1 (Gpr37l1), mRNA. 11/22Length = 2451	ESTs
2586	20515	NM_145784	II	Rattus norvegicus G protein-coupled receptor 37-like 1 (Gpr37l1), mRNA. 11/22Length = 2451	ESTs
2586	19976	NM_145784	jj,kk	Rattus norvegicus G protein-coupled receptor 37-like 1 (Gpr37l1), mRNA. 11/22Length = 2451	ESTs
2586	20046	NM_145784	w,x	Rattus norvegicus G protein-coupled receptor 37-like 1 (Gpr37l1), mRNA. 11/22Length = 2451	ESTs
2587	20740	NM_145878	d,j,k,t,bb,gg,kk, ll	Rattus norvegicus fatty acid binding protein 5, epidermal (Fabp5), mRNA. 11/22Length = 664	Rattus norvegicus Sprague-Dawley lipid-binding protein mRNA, complete cds
2588	5095	NM_147140	u,v	Rattus norvegicus PLRR-4 polymorphic leucine-rich repeat protein (Plrr4), mRNA. 11/22Length = 2275	Rattus norvegicus clone PLRR-4 polymorphic leucine-rich repeat protein mRNA, complete cds
2589	25435	NM_147208	s,t	Rattus norvegicus ischemia related factor vof-21 (LOC259228), mRNA. 11/22Length = 4885	

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2590	90	NM_147210	h,l	Rattus norvegicus nuclear receptor subfamily 1, group D, member 2 (Nr1d2), mRNA. 11/22Length = 1996	Rattus norvegicus nuclear receptor Rev-Erba-beta mRNA, partial cds
2591	1760	NM_147211	d,kk	Rattus norvegicus SH3 domain binding protein CR16 (CR16), mRNA. 11/22Length = 4359	Rattus norvegicus SH3 domain binding protein (CR16) mRNA, complete cds
2592	10544	NM_152935	s,t,u,v	Rattus norvegicus outer mitochondrial membrane receptor rTOM2 (LOC26661), mRNA. 11/22Length = 976	Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
2593	12700	NM_152936	h,l	Rattus norvegicus pancreatic secretory trypsin inhibitor type II (PSTI-II) (LOC26662), mRNA. 11/22Length = 379	Rat pancreatic secretory trypsin inhibitor type II (PSTI-II) mRNA, complete cds
2594	15711	NM_153629	p	Rattus norvegicus heat shock 7 kDa protein 4 (Hspa4), mRNA. 1/22Length = 4521	Rattus norvegicus ischemia responsive 94 kDa protein (irp94) mRNA, complete cds
2595	4834	NM_153821	h,l	Rattus norvegicus paired mesoderm homeobox 1 (Pmx1), mRNA. 1/22Length = 1375	ESTs, ESTs, Highly similar to S37300 glycogen phosphorylase (EC 2.4.1.1), brain - rat [R.norvegicus]
2596	19888	S56464	cc,dd		ESTs
2597	15693	S56679	aa,bb	glutamate receptor, ionotropic, AMPA1 (alpha 1)	glutamate receptor, ionotropic, AMPA1 (alpha 1)
2598	25495	S59892	b,l,m		
2599	25496	S59893	b,l,m		
2600	8210	S61960	jj,kk	ferritin light chain 1	ferritin light chain 1
2601	3244	S63519	a,c,r,w,x		ESTs
2602	951	S69206	ii	mast cell protease 1	mast cell protease 1
2603	18647	S69316	d,e		ESTs, Weakly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
2604	25066	S75280	r		
2605	25538	S76466	gg		
2606	24469	S77858	ll		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
2607	21583	S77900	bb,kk		ESTs, Highly similar to A37100 myosin regulatory light chain A, smooth muscle - rat [R.norvegicus]
2607	25545	S77900	jj,kk		
2608	17626	S78556	gg		ESTs, Highly similar to I56581 dnaK-type molecular chaperone grp75 precursor - rat [R.norvegicus]
2608	25547	S78556	n,cc,dd,ll		
2609	25550	S79213	d	protein phosphatase 1, regulatory (inhibitor) subunit 2	
2610	25556	S79939	hh		
2611	25571	S98336	u,v		
2612	25075	U01347	l,m		
2613	25572	U02534	b		
2614	15462	U06230	f,g	protein S	protein S
2615	16675	U17565	r,li	mini chromosome maintenance deficient 6 (S. cerevisiae)	mini chromosome maintenance deficient 6 (S. cerevisiae)
2616	25589	U21718	d,hh		
2617	22196	U21719	d		ESTs
2618	25590	U21720	hh		
2619	298	U25282	b,l,m		
2620	25593	U26310	gg	tensin	



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2621	399	U31668	p,q	E2F transcription factor 5	E2F transcription factor 5
2622	20224	U47014	b,u,v	proprotein convertase subtilisin/kexin type 5	proprotein convertase subtilisin/kexin type 5
2623	14554	U48828	ll		R.norvegicus H1SHR mRNA, Rattus norvegicus retroviral-like ovarian specific transcript 30-1 mRNA
2624	21654	U53184	a,e,j,k,q,y,z,kk	LPS-induced TNF-alpha factor	LPS-induced TNF-alpha factor
2625	1283	U61729	cc,dd,ll		Rattus norvegicus proline rich protein mRNA, complete cds
2626	25618	U64705	r		
2626	25619	U64705	r		
2627	20386	U68562	cc,dd	heat shock protein 60 (liver)	heat shock protein 60 (liver)
2628	25629	U70270	n,o		
2629	1715	U72660	a,jj,kk	Ninjurin	Ninjurin
2630	2153	U75404	u,v	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein (gravin) 12
2631	25632	U75405	g		
2632	25638	U75923	gg	isoleucine-tRNA synthetase	
2633	17296	U76206	jj,kk	G protein-coupled receptor VTR 15-20	G protein-coupled receptor VTR 15-20
2634	25643	U77829	cc,dd	growth arrest specific 5	
2634	4477	U77829	d	growth arrest specific 5	ESTs
2635	25647	U83119	g,gg		
2636	983	U89745	u,ii	unknown protein	
2637	23282	U90725	hh	lipoprotein-binding protein	lipoprotein-binding protein
2638	25659	U95157	b,l,m	ryanodine receptor type II	
2639	20818	X02904	ii	glutathione S-transferase, pi 2	glutathione S-transferase, pi 2
2640	20169	X03347	p,q		
2641	10181	X06769	p,q	FBJ murine osteosarcoma viral (v-fos) oncogene homolog	FBJ murine osteosarcoma viral (v-fos) oncogene homolog
2642	14966	X07551	c,w,x,cc,dd		
2643	25671	X07686	g		
2644	2464	X13411	u,v	Eph receptor B2 (ELK-related protein tyrosine kinase)	Eph receptor B2 (ELK-related protein tyrosine kinase)
2645	20810	X14181	f,g,w,x		ESTs, Highly similar to R5RT18 ribosomal protein L18a, cytosolic [validated] - rat [R.norvegicus]
2646	18541	X14671	g		ESTs, Highly similar to RL26_RAT 60S RIBOSOMAL PROTEIN L26 [R.norvegicus]
12	21152	X14848	bb	Rattus norvegicus mitochondrial genome. 9/22Length = 16,3	golgi SNAP receptor complex member 1
2647	19244	X15013	f,g,w,x		ESTs, Highly similar to RL7A_HUMAN 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypeptide) [R.norvegicus]
2647	25679	X15013	f,g,aa		
2648	15626	X17665	w,x	ribosomal protein S16	ESTs, Highly similar to R3RT16 ribosomal protein S16, cytosolic [validated] - rat [R.norvegicus]
2649	10819	X51536	gg	ribosomal protein S3	ESTs, Highly similar to RS3_MOUSE 40S ribosomal protein S3 [R.norvegicus]
2649	25686	X51536	w,x,hh	ribosomal protein S3	
2650	18250	X51706	w,x	ribosomal protein L9	ESTs, Highly similar to RL9_RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus]
2651	20872	X51707	l,w,x	ribosomal protein S19	ESTs, Highly similar to R3RT19 ribosomal protein S19, cytosolic [validated] - rat [R.norvegicus]
2652	16715	X53054	cc,dd,ii		Rat mRNA for RT1.D beta chain
2652	16716	X53054	c		Rat mRNA for RT1.D beta chain
2653	20427	X53378	h	ribosomal protein S13	ribosomal protein S13

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2654	18606	X53504	g,w,x		ESTs, Highly similar to RL12_RAT 60S RIBOSOMAL PROTEIN L12 [R.norvegicus]
2654	25691	X53504	g		
2655	25692	X53581	hh		
2655	20617	X53581	g		
2656	1037	X57523	d	Transporter 1, ABC (ATP binding cassette)	Transporter 1, ABC (ATP binding cassette)
2657	15106	X57529	h,l,aa		ESTs, Highly similar to RS18_HUMAN 40S ribosomal protein S18 (KE-3) (KE3) [R.norvegicus]
2658	18611	X58200	g	ribosomal protein L29	ribosomal protein L29
2658	5667	X58200	h,l,w,x	ribosomal protein L23	
2659	25702	X58465	g,w,x	Ribosomal protein S5	Ribosomal protein S5
2659	10109	X58465	g,w,x	Ribosomal protein S5	Ribosomal protein S5
2660	25705	X59375	b,d,l,kk		
2661	25710	X59864	ll		
2662	17176	X60212	f		R.norvegicus ASI mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22
2663	25711	X60468	s,t	amyloid beta (A4) precursor protein-binding, family B, member 1	amyloid beta (A4) precursor protein-binding, family B, member 1
2664	25716	X61295	c,g,hh		
2665	21657	X61381	d,j,k,m,y,z,kk		Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
2666	15875	X62145	h,r	ribosomal protein L8	ESTs, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [R.norvegicus]
2667	13646	X62166	n,o,w,x,kk,ll		ESTs, Highly similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus]
2668	15387	X62482	w,x		ESTs, Highly similar to R3RT25 ribosomal protein S25, cytosolic [validated] - rat [R.norvegicus]
2669	16780	X62660	c,f,g	HMM:glutathione S-transferase, alpha 4	ESTs, Highly similar to S23433 glutathione transferase (EC 2.5.1.18) 8 - rat [R.norvegicus]
2670	25090	X63594	j,k	Inhibitor of nuclear factor of kappa light chain gene enhancer in B-cells, alpha	
2671	20844	X65228	f,g,cc,dd		ESTs, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat [R.norvegicus]
2672	436	X67877	c,s,t,gg		R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein
2673	602	X68101	ee,ff		R.norvegicus trg mRNA
2674	16426	X70369	c,g,bb	procollagen, type III, alpha 1	procollagen, type III, alpha 1
2675	25737	X70667	l,m	melanocortin 3 receptor	
2676	16725	X73371	e,jj,kk		R.norvegicus mRNA for Fc gamma receptor
2677	24232	X75207	aa,bb	Cyclin D1	Cyclin D1
2678	16272	X76456	u,v		
2679	25741	X76489	s,t	CD9 antigen (p24)	
2680	25094	X77117	bb		
2681	25743	X80130	aa,bb		
2682	18621	X82669	ii	RT1 class Ib gene	RT1 class Ib gene
2683	25752	X89694	b,l,m		
2684	25761	X89702	j,k		
2685	25765	X89706	b,c,u,v		
2686	18031	X94551	f,r	laminin, gamma 1	laminin, gamma 1
2687	12978	X96437	a,j,k,p,q,y,z,ee,ff		ESTs, Highly similar to S33363 gly96 protein - mouse [M.musculus]
2687	25770	X96437	b,c,u,v,y		
2688	19279	Y00350	a,aa,bb,jj,kk	uroporphyrinogen decarboxylase	uroporphyrinogen decarboxylase

TABLE 1					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2689	17146	Y07534	aa	Serine protease inhibitor	Serine protease inhibitor
2690	25777	Y08355	l,m	oxidative stress induced	oxidative stress induced
2691	18352	Z12298	aa,bb	decorin	decorin
2692	25790	Z21935	b,u,v	mitogen activated protein kinase 4	
2693	19694	Z48444	cc,dd	A disintegrin and metalloprotease domain (ADAM) 10	A disintegrin and metalloprotease domain (ADAM) 10
2694	17481	Z49761	w,x		R.norvegicus mRNA for RT1.Ma
2695	8664	Z75029	y,z,ee,ff		ESTs, Moderately similar to T17342 hypothetical protein DKFZp586K1924.1 - human (fragment) [H.sapiens], R.norvegicus hsp70.2 mRNA for heat shock protein 70
2696	15569	Z78279	c,g,bb	procollagen, type I, alpha 1	procollagen, type I, alpha 1
2696	15570	Z78279	c,f,g,j,k	procollagen, type I, alpha 1	procollagen, type I, alpha 1

TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
1649	20127	AJ011116	j, k, n, o	Actions of Nitric Oxide in the Heart, Arginine and proline metabolism, Hypoxia-Inducible Factor in the Cardiovascular System
2037	18569	NM_019212	f, w, x, hh	Actions of Nitric Oxide in the Heart, Integrin Signaling Pathway
2284	25795	NM_031556	jj, kk	Actions of Nitric Oxide in the Heart, Integrin Signaling Pathway
2019	15975	NM_019132	ii	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor, Activation of cAMP-dependent protein kinase, PKA, Attenuation of GPCR Signaling, CCR3 signaling in Eosinophils, ChREBP regulation by carbohydrates and cAMP, Erk1/Erk2 Mapk Signaling pathway, Phospholipase C-epsilon pathway, Signaling Pathway from G-Protein Families, Transcription factor CREB and its extracellular signals
1835	2555	NM_012967	a, y, z, kk	Adhesion Molecules on Lymphocyte, B Lymphocyte Cell Surface Molecules, CTL mediated immune response against target cells, Cells and Molecules involved in local acute inflammatory response, Monocyte and its Surface Molecules, Neutrophil and its Surface Molecules, T Cytotoxic Cell Surface Molecules, T Helper Cell Surface Molecules
1356	14989	AI177366	f, g, l, m, kk	Adhesion Molecules on Lymphocyte, Cells and Molecules involved in local acute inflammatory response, Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Monocyte and its Surface Molecules, PTEN dependent cell cycle arrest and apoptosis, Ras-Independent pathway in NK cell-mediated cytotoxicity
1826	1625	NM_012924	gg	Adhesion Molecules on Lymphocyte, Monocyte and its Surface Molecules, Neutrophil and its Surface Molecules
2670	25090	X63594	j, k	AKT Signaling Pathway, ATM Signaling Pathway, Acetylation and Deacetylation of RelA in The Nucleus, Activation of PKC through G protein coupled receptor, CD40L Signaling Pathway, Double Stranded RNA Induced Gene Expression, Erythropoietin mediated neuroprotection through NF-kB, HIV-1 Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors, Influence of Ras and Rho proteins on G1 to S Transition, NF-kB Signaling Pathway, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells, Signal transduction through IL1R, T Cell Receptor Signaling Pathway, TNF/Stress Related Signaling, TNFR2 Signaling Pathway, The 41BB-dependent immune response, Toll-Like Receptor Pathway, interact6-1
1918	3203	NM_017039	c	AKT Signaling Pathway, ChREBP regulation by carbohydrates and cAMP, Erk1/Erk2 Mapk Signaling pathway, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Regulation of ck1/cdk5 by type 1 glutamate receptors, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, WNT Signaling Pathway, mTOR Signaling Pathway
815	17524	AI010568	jj, kk	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of eIF4e and p70 S6 Kinase
1936	10886	NM_017094	ii	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of eIF4e and p70 S6 Kinase
1936	10887	NM_017094	jj, kk	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of eIF4e and p70 S6 Kinase
1936	10888	NM_017094	e, r, hh	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of eIF4e and p70 S6 Kinase
2082	23424	NM_021680	j, k	Alanine and aspartate metabolism, Aminoacyl-tRNA biosynthesis
1785	1478	NM_012744	n, o	Alanine and aspartate metabolism, Citrate cycle (TCA cycle), Pyruvate metabolism
2028	7486	NM_019169	n, o	Alpha-synuclein and Parkin-mediated proteolysis in Parkinson's disease, Role of Parkin in Ubiquitin-Proteasomal Pathway
143	16756	AA818089	ll	Aminoacyl-tRNA biosynthesis, Glycine, serine and threonine metabolism
450	12031	AA893860	y, z	Aminoacyl-tRNA biosynthesis, Glycine, serine and threonine metabolism

TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
1376	6502	AI178283	r	Aminoacyl-tRNA biosynthesis, Phenylalanine, tyrosine and tryptophan biosynthesis
2426	7927	NM_053765	d	Aminosugars metabolism
1748	619	NM_012565	l, m, n, o	Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism
2093	17100	NM_022179	h, l, w, x, dd	Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism
1771	21087	NM_012661	cc, dd	Androgen and estrogen metabolism
2195	25070	NM_024392	r, ii	Androgen and estrogen metabolism
2477	15125	NM_057105	jj, kk, ll	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
2510	17564	NM_133283	hh	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Anthrax Toxin Mechanism of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
1924	910	NM_017059	d	Apoptotic Signaling in Response to DNA Damage, Hypoxia and p53 in the Cardiovascular system, Regulation of BAD phosphorylation, Role of Mitochondria in Apoptotic Signaling, p53 Signaling Pathway
1924	911	NM_017059	d	Apoptotic Signaling in Response to DNA Damage, Hypoxia and p53 in the Cardiovascular system, Regulation of BAD phosphorylation, Role of Mitochondria in Apoptotic Signaling, p53 Signaling Pathway
1924	912	NM_017059	d, l, m	Apoptotic Signaling in Response to DNA Damage, Hypoxia and p53 in the Cardiovascular system, Regulation of BAD phosphorylation, Role of Mitochondria in Apoptotic Signaling, p53 Signaling Pathway
602	22283	AA945172	e	Arginine and proline metabolism
2214	15682	NM_031011	n, o	Arginine and proline metabolism
2214	15683	NM_031011	cc, dd, gg	Arginine and proline metabolism
119	11901	AA801058	d	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
1988	20913	NM_017272	n, o	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
2118	20915	NM_022407	kk	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism

TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
2353	12299	NM_032416	c	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
1296	19118	AI175281	hh	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups
1798	16947	NM_012793	b, u, v, jj, kk	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups
1842	19393	NM_012998	h, l	Arginine and proline metabolism, Hypoxia-Inducible Factor in the Cardiovascular System
1739	4467	NM_012529	f, g	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
1739	4468	NM_012529	g	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
1862	13283	NM_013078	b	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
2128	4242	NM_022521	b, l, m	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
2089	22351	NM_021835	ee, ff	ATM Signaling Pathway, Angiotensin II mediated activation of JNK1 pathway via Pyk2 dependent signaling, BCR Signaling Pathway, D4-GDI Signaling Pathway, EGF Signaling Pathway, EPO Signaling Pathway, FAS signaling pathway ( CD95 ), Fc Epsilon Receptor I Signaling in Mast Cells, Hypoxia-Inducible Factor in the Cardiovascular System, IGF-1 Signaling Pathway, IL 2 signaling pathway, IL 6 signaling pathway, Inhibition of Cellular Proliferation by Gleevec, Insulin Signaling Pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Nerve growth factor pathway (NGF), PDGF Signaling Pathway, Pertussis toxin-insensitive CCR5 Signaling in Macrophage, Repression of Pain Sensation by the Transcriptional Regulator DREAM, Signal transduction through IL1R, Signaling Pathway from G-Protein Families, T Cell Receptor Signaling Pathway, TNF/Stress Related Signaling, TNFR1 Signaling Pathway, TPO Signaling Pathway, TSP-1 Induced Apoptosis in Microvascular Endothelial Cell, The 41BB-dependent immune response, Toll-Like Receptor Pathway,
2173	352	NM_024127	p, q	ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway
2173	353	NM_024127	q, ee, ff, gg	ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway
2173	354	NM_024127	p, q, ee, ff	ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway
1205	17914	AI169159	hh	ATP Synthesis, Oxidative phosphorylation
1209	22661	AI169265	gg	ATP Synthesis, Oxidative phosphorylation
2000	16844	NM_017311	n, o	ATP Synthesis, Oxidative phosphorylation
2327	16178	NM_031785	f	ATP Synthesis, Oxidative phosphorylation
2448	20939	NM_053884	gg	ATP Synthesis, Oxidative phosphorylation
2566	17203	NM_139099	g, hh	ATP Synthesis, Oxidative phosphorylation
2566	17204	NM_139099	g	ATP Synthesis, Oxidative phosphorylation

TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
1319	10182	AI176185	p, q, gg	BCR Signaling Pathway, EGF Signaling Pathway, EPO Signaling Pathway, Fc Epsilon Receptor I Signaling in Mast Cells, IGF-1 Signaling Pathway, IL 2 signaling pathway, IL 3 signaling pathway, IL 6 signaling pathway, IL-2 Receptor B Protein Interaction Pathway, Inhibition of Cellular Proliferation by Gleevec, Insulin Signaling Pathway, Nerve growth factor pathway (NGF), PDGF Signaling Pathway, Pertussis toxin-insensitive CCR5 Signaling in Macrophage, Repression of Pain Sensation by the Transcriptional Regulator DREAM, Signaling Pathway from G-Protein Families, T Cell Receptor Signaling Pathway, TPO Signaling Pathway, TSP-1 Induced Apoptosis in Microvascular Endothelial Cell, Toll-Like Receptor Pathway, egf, epo, igf-1, il2, il3, il6, insulin, ngf, pdgf, tpo
2641	10181	X06769	p, q	BCR Signaling Pathway, EGF Signaling Pathway, EPO Signaling Pathway, Fc Epsilon Receptor I Signaling in Mast Cells, IGF-1 Signaling Pathway, IL 2 signaling pathway, IL 3 signaling pathway, IL 6 signaling pathway, IL-2 Receptor B Protein Interaction Pathway, Inhibition of Cellular Proliferation by Gleevec, Insulin Signaling Pathway, Nerve growth factor pathway (NGF), PDGF Signaling Pathway, Pertussis toxin-insensitive CCR5 Signaling in Macrophage, Repression of Pain Sensation by the Transcriptional Regulator DREAM, Signaling Pathway from G-Protein Families, T Cell Receptor Signaling Pathway, TPO Signaling Pathway, TSP-1 Induced Apoptosis in Microvascular Endothelial Cell, Toll-Like Receptor Pathway, egf, epo, igf-1, il2, il3, il6, insulin, ngf, pdgf, tpo
1930	18956	NM_017075	aa	Benzoate degradation, Bile acid biosynthesis, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Synthesis and degradation of ketone bodies, Tryptophan metabolism
1930	18957	NM_017075	r, s, t, ll	Benzoate degradation, Bile acid biosynthesis, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Synthesis and degradation of ketone bodies, Tryptophan metabolism
1150	23596	AI105435	bb	Benzoate degradation, Fatty acid metabolism, Lysine degradation, Tryptophan metabolism
1732	23698	NM_012489	l	Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Valine, leucine and isoleucine degradation
280	16074	AA874874	p, q	Bile acid biosynthesis, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Methane metabolism, Pyruvate metabolism, Tyrosine metabolism
1781	25563	NM_012732	f, g	Bile acid biosynthesis, Glycerolipid metabolism
1781	16613	NM_012732	g	Bile acid biosynthesis, Glycerolipid metabolism
1970	13938	NM_017212	jj, kk	Bioactive Peptide Induced Signaling Pathway
1970	13940	NM_017212	a	Bioactive Peptide Induced Signaling Pathway
2276	12580	NM_031514	a, h, l, j, k, y, z	Bioactive Peptide Induced Signaling Pathway, EPO Signaling Pathway, Erythropoietin mediated neuroprotection through NF-kB, Growth Hormone Signaling Pathway, IFN gamma signaling pathway, IL 3 signaling pathway, IL 6 signaling pathway, IL22 Soluble Receptor Signaling Pathway, Inhibition of Cellular Proliferation by Gleevec, Stat3 Signaling Pathway, TPO Signaling Pathway, epo, ifn_gamma, il3, il6, interact6-1, pdgf, tpo
2276	12581	NM_031514	y, z, hh	Bioactive Peptide Induced Signaling Pathway, EPO Signaling Pathway, Erythropoietin mediated neuroprotection through NF-kB, Growth Hormone Signaling Pathway, IFN gamma signaling pathway, IL 3 signaling pathway, IL 6 signaling pathway, IL22 Soluble Receptor Signaling Pathway, Inhibition of Cellular Proliferation by Gleevec, Stat3 Signaling Pathway, TPO Signaling Pathway, epo, ifn_gamma, il3, il6, interact6-1, pdgf, tpo
133	23828	AA817823	ii	Blood group glycolipid biosynthesis - neolact series, Galactose metabolism, Keratan sulfate biosynthesis, N-Glycans biosynthesis

TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
412	11997	AA892828	f, h, l	Butanoate metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism, Valine, leucine and isoleucine biosynthesis
1313	5876	AI176117	hh	Butanoate metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism, Valine, leucine and isoleucine biosynthesis
2541	8692	NM_134387	hh	Butanoate metabolism, Pentose and glucuronate interconversions
1987	20600	NM_017268	ii	Butanoate metabolism, SREBP and controls lipid synthesis, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
1987	20601	NM_017268	r	Butanoate metabolism, SREBP and controls lipid synthesis, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
2465	17739	NM_053995	g	Butanoate metabolism, Synthesis and degradation of ketone bodies
2193	2811	NM_024386	cc, dd	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
2193	2812	NM_024386	w, x, cc, dd	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
2193	2813	NM_024386	b	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
1587	18151	AI237212	f, g, hh	Calcium Signaling by HBx of Hepatitis B virus
2126	162	NM_022516	e, u, v	Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO <sub>2</sub> fixation)
2365	1311	NM_053291	e	Carbon fixation, Glycolysis / Gluconeogenesis, Glycolysis Pathway
873	20086	AI013260	z	Caspase Cascade in Apoptosis, FAS signaling pathway ( CD95 ), HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors , TNFR1 Signaling Pathway
544	5206	AA925755	ll	Catabolic Pathways for Arginine , Histidine, Glutamate, Glutamine, and Proline, D-Glutamine and D-glutamate metabolism, Glutamate metabolism, Nitrogen metabolism
1850	1338	NM_013022	r	CCR3 signaling in Eosinophils
1952	15364	NM_017147	ii	CCR3 signaling in Eosinophils, Rac 1 cell motility signaling pathway, Rho cell motility signaling pathway
1952	15365	NM_017147	aa, bb, ll	CCR3 signaling in Eosinophils, Rac 1 cell motility signaling pathway, Rho cell motility signaling pathway
2427	15996	NM_053769	cc, dd	CD40L Signaling Pathway, Phosphatidylinositol signaling system, TNFR2 Signaling Pathway
1658	17264	D25233	d	Cell Cycle: G1/S Check Point , Cyclin E Destruction Pathway, Cyclins and Cell Cycle Regulation, E2F1 Destruction Pathway, FAS signaling pathway ( CD95 ), HIV-I Nef: negative effector of Fas and TNF, Influence of Ras and Rho proteins on G1 to S Transition, Overview of telomerase RNA component gene hTerc Transcriptional Regulation, RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage, Regulation of p27 Phosphorylation during Cell Cycle Progression, TNFR1 Signaling Pathway, p53 Signaling Pathway
1657	25041	D14014	f	Cell Cycle: G1/S Check Point , Cyclins and Cell Cycle Regulation, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Influence of Ras and Rho proteins on G1 to S Transition, WNT Signaling Pathway, p53 Signaling Pathway
2677	24232	X75207	aa, bb	Cell Cycle: G1/S Check Point , Cyclins and Cell Cycle Regulation, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Influence of Ras and Rho proteins on G1 to S Transition, WNT Signaling Pathway, p53 Signaling Pathway
2079	18729	NM_021578	r	Cell Cycle: G1/S Check Point , Cytokines and Inflammatory Response, Erythrocyte Differentiation Pathway, Function of SLRP in Bone: An Integrated View, Selective expression of chemokine receptors during T-cell polarization, Signal transduction through IL1R, TGF beta signaling pathway, p38 MAPK Signaling Pathway , tgf-beta



TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
73	13683	AA799788	e	Cell Cycle: G2/M Checkpoint, Cyclin E Destruction Pathway, E2F1 Destruction Pathway
1702	13682	L38482	e	Cell Cycle: G2/M Checkpoint, Cyclin E Destruction Pathway, E2F1 Destruction Pathway
2212	21166	NM_031005	a, n, o	Cell to Cell Adhesion Signaling, Integrin Signaling Pathway
1755	24716	NM_012589	j, k, p, q	Cells and Molecules involved in local acute inflammatory response, Cytokine Network, Cytokines and Inflammatory Response, Erythrocyte Differentiation Pathway, IL 17 Signaling Pathway, IL 5 Signaling Pathway, IL 6 signaling pathway, Regulation of hematopoiesis by cytokines, Signal transduction through IL1R, il6, interact6-1
875	6758	AI013394	d, jj, kk	Chondroitin / Heparan sulfate biosynthesis
2275	17427	NM_031510	b, u, v	Citrate cycle (TCA cycle), Glutathione metabolism, Reductive carboxylate cycle (CO2 fixation)
2425	18175	NM_053752	aa, bb	Citrate cycle (TCA cycle), Propanoate metabolism
2363	25072	NM_052807	j, k	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Erk1/Erk2 Mapk Signaling pathway, IGF-1 Signaling Pathway, Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation, Regulation of BAD phosphorylation, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, igf-1
1915	17807	NM_017025	h, l	Cysteine metabolism, Glycolysis / Gluconeogenesis, Hypoxia-Inducible Factor in the Cardiovascular System, Propanoate metabolism, Pyruvate metabolism
1757	7125	NM_012595	aa, bb	Cysteine metabolism, Glycolysis / Gluconeogenesis, Propanoate metabolism, Pyruvate metabolism
2017	20318	NM_019127	n, o	Cytokine Network, Cytokines and Inflammatory Response, Dendritic cells in regulating TH1 and TH2 Development, IFN alpha signaling pathway, Signal transduction through IL1R
872	1332	AI013222	e	Cytokines and Inflammatory Response, PDGF Signaling Pathway, pdgf
1910	8417	NM_017008	aa	D-Arginine and D-ornithine metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway
1583	22939	AI236669	y, z, jj, kk	DNA polymerase, Purine metabolism, Pyrimidine metabolism
1951	24106	NM_017141	s, t, bb	DNA polymerase, Purine metabolism, Pyrimidine metabolism
1951	24107	NM_017141	ll	DNA polymerase, Purine metabolism, Pyrimidine metabolism
470	24329	AA899253	aa, bb	Effects of calcinurin in Keratinocyte Differentiation
1784	25650	NM_012736	d	Electron -Transfer Reaction in Mitochondria, Glycerolipid metabolism
1759	2628	NM_012603	a, p, q, y, z	Erk1/Erk2 Mapk Signaling pathway, IL-2 Receptor B Protein Interaction Pathway, Inhibition of Cellular Proliferation by Gleevec, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells, Overview of telomerase protein component gene hTert Transcriptional Regulation , WNT Signaling Pathway, p38 MAPK Signaling Pathway
1759	2629	NM_012603	a, j, k, p, q, y, z, ee, ff, kk	Erk1/Erk2 Mapk Signaling pathway, IL-2 Receptor B Protein Interaction Pathway, Inhibition of Cellular Proliferation by Gleevec, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells, Overview of telomerase protein component gene hTert Transcriptional Regulation , WNT Signaling Pathway, p38 MAPK Signaling Pathway
1761	1298	NM_012610	d	Erk1/Erk2 Mapk Signaling pathway, Nerve growth factor pathway (NGF), Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway, ngf
1761	1299	NM_012610	cc, dd	Erk1/Erk2 Mapk Signaling pathway, Nerve growth factor pathway (NGF), Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway, ngf
1911	24676	NM_017010	aa, bb	Erythropoietin mediated neuroprotection through NF-kB
2188	1146	NM_024359	y, z	Erythropoietin mediated neuroprotection through NF-kB, Hypoxia and p53 in the Cardiovascular system, Hypoxia-Inducible Factor in the Cardiovascular System

TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
2004	24248	NM_017332	e, gg	Fatty acid biosynthesis (path 1)
431	20985	AA893242	ll	Fatty acid metabolism
431	20986	AA893242	ll	Fatty acid metabolism
972	20983	AI044900	a, h, l, ee, ff, kk	Fatty acid metabolism
1652	18686	D00729	g, hh	Fatty acid metabolism
1668	20984	D90109	ll	Fatty acid metabolism
1999	18687	NM_017306	hh	Fatty acid metabolism
2410	13005	NM_053623	j, k, y, z	Fatty acid metabolism
1896	20855	NM_013200	a, w, x, hh	Fatty acid metabolism, Glycerolipid metabolism
1896	20856	NM_013200	a, w, x, aa, hh, ll	Fatty acid metabolism, Glycerolipid metabolism
1827	1977	NM_012930	a, w, x, cc, dd	Fatty acid metabolism, Glycerolipid metabolism, Mitochondrial Carnitine Palmitoyltransferase (CPT) System
1708	20714	M14972	s, t	Fatty acid metabolism, Tryptophan metabolism
1743	20704	NM_012541	aa, bb	Fatty acid metabolism, Tryptophan metabolism
1831	190	NM_012940	j, k	Fatty acid metabolism, Tryptophan metabolism
1832	20928	NM_012941	l, m	Fatty acid metabolism, Tryptophan metabolism
1909	20921	NM_016999	s, t	Fatty acid metabolism, Tryptophan metabolism
2030	1174	NM_019184	c	Fatty acid metabolism, Tryptophan metabolism
2281	4010	NM_031543	u, v	Fatty acid metabolism, Tryptophan metabolism
2281	4011	NM_031543	v	Fatty acid metabolism, Tryptophan metabolism
2528	244	NM_133551	a, j, k, y, z, ee, ff, kk	Fc Epsilon Receptor I Signaling in Mast Cells, Glycerolipid metabolism, Phospholipid degradation, Prostaglandin and leukotriene metabolism, p38 MAPK Signaling Pathway
2398	19252	NM_053576	a	Flavonoids, stilbene and lignin biosynthesis, Methane metabolism, Phenylalanine metabolism
1718	21400	M36410	ee, ff, gg	Folate biosynthesis
2109	13480	NM_022390	l	Folate biosynthesis
2187	15349	NM_024356	a, y, z	Folate biosynthesis
2187	15353	NM_024356	j, k, y, z, ii	Folate biosynthesis
1858	14997	NM_013059	e, ee, ff	Folate biosynthesis, Glycerolipid metabolism
1971	1527	NM_017220	ee, ff	Folate biosynthesis, Nicotinate and nicotinamide metabolism, Purine metabolism, Pyrimidine metabolism
1922	20875	NM_017050	hh	Free Radical Induced Apoptosis
1922	20876	NM_017050	r	Free Radical Induced Apoptosis
2202	1852	NM_030826	aa, gg	Free Radical Induced Apoptosis, Glutathione metabolism
1956	21975	NM_017154	d, e, j, k, n, o, y, z, kk	Free Radical Induced Apoptosis, Purine metabolism
1923	1876	NM_017052	w, x	Fructose and mannose metabolism
2060	1238	NM_019333	gg	Fructose and mannose metabolism
1733	15511	NM_012498	ii	Fructose and mannose metabolism, Galactose metabolism, Glycerolipid metabolism, Pentose and glucuronate interconversions, Pyruvate metabolism
1701	12058	L25387	w	Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
1701	25377	L25387	hh	Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
2320	1340	NM_031715	jj, kk	Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
2693	19694	Z48444	cc, dd	Generation of amyloid b-peptide by PS1
1998	14004	NM_017305	aa, bb	Glutamate metabolism, Glutathione metabolism
1929	11152	NM_017073	c, s, t, kk	Glutamate metabolism, Nitrogen metabolism
1929	11153	NM_017073	y, kk	Glutamate metabolism, Nitrogen metabolism
938	7867	AI043695	t	Glutamate metabolism, Purine metabolism

TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
658	23927	AA957007	g	Glutathione metabolism
1799	961	NM_012796	g	Glutathione metabolism
1912	21013	NM_017014	b	Glutathione metabolism
1958	17686	NM_017165	hh	Glutathione metabolism
2131	4615	NM_022525	cc, dd	Glutathione metabolism
2265	20862	NM_031154	w, x	Glutathione metabolism
2274	25525	NM_031509	b, r	Glutathione metabolism
2274	634	NM_031509	d, r	Glutathione metabolism
2274	635	NM_031509	d, r	Glutathione metabolism
2639	20818	X02904	ii	Glutathione metabolism
2669	16780	X62660	c, f, g	Glutathione metabolism
1885	200	NM_013161	b, l, m	Glycerolipid metabolism
1989	20281	NM_017274	gg	Glycerolipid metabolism
2380	14621	NM_053437	e, hh	Glycerolipid metabolism
2260	1638	NM_031143	d, e, ii, kk	Glycerolipid metabolism, Phosphatidylinositol signaling system
1962	9378	NM_017174	jj, kk	Glycerolipid metabolism, Phospholipid degradation, Prostaglandin and leukotriene metabolism
1758	18386	NM_012598	w, x	Glycerolipid metabolism, Visceral Fat Deposits and the Metabolic Syndrome
1758	18387	NM_012598	w, x	Glycerolipid metabolism, Visceral Fat Deposits and the Metabolic Syndrome
1844	24718	NM_013003	ii	Glycine, serine and threonine metabolism
1894	16448	NM_013197	b, c, v	Glycine, serine and threonine metabolism
2003	24533	NM_017328	n, o	Glycolysis / Gluconeogenesis
2343	24644	NM_031972	cc, dd	Glycolysis / Gluconeogenesis, Histidine metabolism, Phenylalanine metabolism, Tyrosine metabolism
1913	17815	NM_017015	w, x	Glycosaminoglycan degradation, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
2073	574	NM_019905	a, h, l, z, aa, kk, ll	Glyoxylate and dicarboxylate metabolism
1726	5733	M81855	d	Hypoxia and p53 in the Cardiovascular system
1754	15098	NM_012588	bb	Hypoxia and p53 in the Cardiovascular system
2309	18403	NM_031677	d, jj, kk	Hypoxia and p53 in the Cardiovascular system
2409	20243	NM_053615	aa, bb	Hypoxia and p53 in the Cardiovascular system, WNT Signaling Pathway
2516	657	NM_133380	j, k, y, z	IL 4 signaling pathway, Selective expression of chemokine receptors during T-cell polarization, Th1/Th2 Differentiation, il4
1914	6598	NM_017020	j, k	IL 6 signaling pathway, il6, interact6-1
2172	21238	NM_024125	p, q	IL 6 signaling pathway, il6, interact6-1
2172	21239	NM_024125	p, q, r, bb, ee, ff, kk	IL 6 signaling pathway, il6, interact6-1
1939	4391	NM_017101	s, t	IL-2 Receptor B Protein Interaction Pathway
1749	482	NM_012567	s, t	Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages
778	3278	AI008988	y, z	Inhibition of Cellular Proliferation by Gleevec, Integrin Signaling Pathway
2092	243	NM_021989	h, l, n, o, ll	Inhibition of Matrix Metalloproteinases
229	17236	AA858903	s, t, gg	Inhibition of Matrix Metalloproteinases, p53 Signaling Pathway
512	17231	AA924107	ii	Inhibition of Matrix Metalloproteinases, p53 Signaling Pathway
697	17232	AA965161	ll	Inhibition of Matrix Metalloproteinases, p53 Signaling Pathway
1891	1714	NM_013187	a, kk	Inositol phosphate metabolism, Phosphatidylinositol signaling system
2186	20933	NM_024353	h, l	Inositol phosphate metabolism, Phosphatidylinositol signaling system
2352	1171	NM_032071	y, z	Inositol phosphate metabolism, Phosphatidylinositol signaling system
260	23336	AA859981	ee, ff, jj, kk	Inositol phosphate metabolism, Phosphatidylinositol signaling system, Streptomycin biosynthesis
2024	20863	NM_019152	cc, dd	Integrin Signaling Pathway
2620	25593	U26310	gg	Integrin Signaling Pathway
1983	1496	NM_017255	aa, bb	Ion Channel and Phorbol Esters Signaling Pathway
1738	15741	NM_012520	ll	Methane metabolism, Tryptophan metabolism

TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
1967	20779	NM_017201	b, l, m	Methionine metabolism, Selenoamino acid metabolism
2277	20448	NM_031530	a, d, z, ee, ff, jj, kk	Msp/Ron Receptor Signaling Pathway, Pertussis toxin-insensitive CCR5 Signaling in Macrophage
2277	20449	NM_031530	a, z, ee, ff, kk	Msp/Ron Receptor Signaling Pathway, Pertussis toxin-insensitive CCR5 Signaling in Macrophage
1318	6782	AI176170	e	mTOR Signaling Pathway
1945	24522	NM_017130	u, v	N-Glycan degradation, Sphingoglycolipid metabolism
2314	21575	NM_031698	w, x	N-Glycans biosynthesis
1874	2005	NM_013127	e, bb	Nicotinate and nicotinamide metabolism
2056	15056	NM_019291	b, c	Nitrogen metabolism
2267	18596	NM_031325	u, v	Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism
2267	18597	NM_031325	a, j, k, p, q, y, z, ee, ff	Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism
299	4339	AA875121	jj, kk	Overview of telomerase RNA component gene hTerc Transcriptional Regulation
1810	4338	NM_012866	u, v	Overview of telomerase RNA component gene hTerc Transcriptional Regulation
1138	23574	AI104520	hh	Oxidative phosphorylation
1712	15049	M24542	aa, bb	Oxidative phosphorylation
1795	449	NM_012786	hh	Oxidative phosphorylation
1795	450	NM_012786	f, hh	Oxidative phosphorylation
1968	14694	NM_017202	aa	Oxidative phosphorylation
2383	21866	NM_053472	u, v	Oxidative phosphorylation
2041	20938	NM_019223	hh	Oxidative phosphorylation, Ubiquinone biosynthesis
2107	11454	NM_022381	d, l, m, n, o, s, t	p53 Signaling Pathway
2107	11455	NM_022381	s	p53 Signaling Pathway
495	23038	AA900881	a, j, k, y, z	Pantothenate and CoA biosynthesis, Valine, leucine and isoleucine biosynthesis, Valine, leucine and isoleucine degradation
2117	24643	NM_022400	b, u, v	Pantothenate and CoA biosynthesis, Valine, leucine and isoleucine biosynthesis, Valine, leucine and isoleucine degradation
269	17742	AA866302	c	Phenylalanine metabolism, Tyrosine metabolism
1468	14430	AI230798	r	Phosphatidylinositol signaling system
1767	1841	NM_012637	d, jj, kk	Phosphatidylinositol signaling system
1767	1844	NM_012637	p, q, y, z	Phosphatidylinositol signaling system
2021	14973	NM_019140	aa	Phosphatidylinositol signaling system
1906	64	NM_016991	jj, kk	Phospholipase C d1 in phospholipid associated cell signaling
1746	23868	NM_012551	a, h, l, p, q, y, z, ee, ff	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
1746	23869	NM_012551	a, h, l, p, q, y, z	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
1746	23871	NM_012551	p, q, y, z, ii	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
1746	23872	NM_012551	p, q, y, z	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
1402	16081	AI179610	a, p, q, r, y, z, gg, kk	Porphyrin and chlorophyll metabolism
1741	16520	NM_012532	c	Porphyrin and chlorophyll metabolism
1751	16080	NM_012580	p, q, y, z, kk	Porphyrin and chlorophyll metabolism
2688	19279	Y00350	a, aa, bb, jj, kk	Porphyrin and chlorophyll metabolism
1976	20193	NM_017232	p, q	Prostaglandin and leukotriene metabolism
2029	17063	NM_019170	f, g	Prostaglandin and leukotriene metabolism
2029	17064	NM_019170	f, g	Prostaglandin and leukotriene metabolism

TABLE 2

Atty. Ref. 44921-5090-01-WO/2105485

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
2029	17066	NM_019170	g	Prostaglandin and leukotriene metabolism
2213	25517	NM_031010	c, v	Prostaglandin and leukotriene metabolism
2213	1845	NM_031010	c, v	Prostaglandin and leukotriene metabolism
2285	692	NM_031557	s, t, ll	Prostaglandin and leukotriene metabolism
190	18673	AA849028	t	Proteasome
1662	9029	D30804	hh	Proteasome
1777	4003	NM_012708	e	Proteasome
1991	15142	NM_017278	l, m	Proteasome
1992	15538	NM_017283	r	Proteasome
2297	11296	NM_031606	f	PTEN dependent cell cycle arrest and apoptosis, Phosphatidylinositol signaling system, Regulation of eIF4e and p70 S6 Kinase, mTOR Signaling Pathway
63	14250	AA799729	j, k	Purine metabolism
1450	23042	AI230130	s, t, ii	Purine metabolism
1762	638	NM_012613	aa, bb	Purine metabolism
1816	16708	NM_012895	u, v	Purine metabolism
1916	14247	NM_017031	h, l	Purine metabolism
2053	8200	NM_019285	ll	Purine metabolism
2229	79	NM_031079	y, z, ee, ff	Purine metabolism
2325	14184	NM_031776	kk	Purine metabolism
2325	14185	NM_031776	kk	Purine metabolism
2299	24234	NM_031614	r, y, z, jj, kk	Pyrimidine metabolism
2299	24235	NM_031614	y, z, kk	Pyrimidine metabolism
2404	20896	NM_053592	h, l	Pyrimidine metabolism
2351	21807	NM_032067	gg	Rac 1 cell motility signaling pathway, Ras Signaling Pathway
2351	21809	NM_032067	ll	Rac 1 cell motility signaling pathway, Ras Signaling Pathway
1423	22845	AI227887	e, aa, bb	Ras Signaling Pathway, Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration, p38 MAPK Signaling Pathway
630	22771	AA946432	b, l, m	Regulation of ck1/cdk5 by type 1 glutamate receptors
2075	18713	NM_020075	p, q, s, t	Regulation of eIF2
2075	18715	NM_020075	ee, ff	Regulation of eIF2
2208	1928	NM_030872	s, t	Regulation of eIF4e and p70 S6 Kinase
2208	1929	NM_030872	hh	Regulation of eIF4e and p70 S6 Kinase
1206	23152	AI169170	r	Regulation of eIF4e and p70 S6 Kinase, mTOR Signaling Pathway
1957	17104	NM_017160	h, l	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR Signaling Pathway
1957	17105	NM_017160	h, l	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR Signaling Pathway
1957	17106	NM_017160	n, o	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR Signaling Pathway
1933	22552	NM_017087	n, o	Small Leucine-rich Proteoglycan (SLRP) molecules
2691	18352	Z12298	aa, bb	Small Leucine-rich Proteoglycan (SLRP) molecules
1236	15393	AI170663	cc, dd	SREBP and controls lipid synthesis
92	4832	AA800190	a, e, ii, kk	Starch and sucrose metabolism
1232	11585	AI170502	r	Starch and sucrose metabolism
2595	4834	NM_153821	h, l	Starch and sucrose metabolism
1948	16681	NM_017136	ii	Sterol biosynthesis, Terpenoid biosynthesis
2251	14970	NM_031127	a, h, l, n, o	Sulfur metabolism
2336	4748	NM_031834	s, t, aa, bb	Sulfur metabolism
2336	4749	NM_031834	t, bb	Sulfur metabolism
1806	17541	NM_012844	c, d	Tetrachloroethene degradation
2162	2006	NM_022936	aa	Tetrachloroethene degradation
2162	2008	NM_022936	w, x, aa, bb	Tetrachloroethene degradation
2033	15244	NM_019191	ll	TGF beta signaling pathway, tgf-beta
2286	18315	NM_031561	e, u	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell

TABLE 2				Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Pathways
2286	18316	NM_031561	e	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
2286	18317	NM_031561	r, aa, bb, ii	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
2286	18319	NM_031561	w, x	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
1740	11115	NM_012531	f, g	Tyrosine metabolism
1740	11116	NM_012531	f, g	Tyrosine metabolism
889	21950	AI013861	a, h, l	Valine, leucine and isoleucine degradation
1688	17285	J02827	c	Valine, leucine and isoleucine degradation
1756	4450	NM_012592	c	Valine, leucine and isoleucine degradation
2577	13712	NM_144744	ii	Visceral Fat Deposits and the Metabolic Syndrome
2035	18572	NM_019201	n, o	WNT Signaling Pathway
2035	18573	NM_019201	f, g	WNT Signaling Pathway

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105486	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2486	15408 NM_057197		f, g, l, m	2,4-dienoyl CoA reductase 1, mitochondrial	2,4-dienoyl CoA reductase 1, mitochondrial	
2486	15409 NM_057197		f, g	2,4-dienoyl CoA reductase 1, mitochondrial	2,4-dienoyl CoA reductase 1, mitochondrial	
1987	20600 NM_017268		ii	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1, 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble), 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2, pre B-cell leukemia transcription factor 1	
1987	20601 NM_017268		r	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1, 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble), 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2, pre B-cell leukemia transcription factor 1	
269	17742 AA866302		c	4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvic acid dioxygenase	4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvic acid dioxygenase	
1753	20313 NM_012585		b, u, v	5-hydroxytryptamine (serotonin) receptor 1A	5-hydroxytryptamine (serotonin) receptor 1A	
1878	786 NM_013148		n, o	5-hydroxytryptamine (serotonin) receptor 5A		
2189	767 NM_024365		b, c	5-hydroxytryptamine (serotonin) receptor 6	5-hydroxytryptamine (serotonin) receptor 6	
1971	1527 NM_017220		ee, ff	6-pyruvoyl-tetrahydropterin synthase, 6-pyruvoyl-tetrahydropterin synthase	6-pyruvoyl-tetrahydropterin synthase, 6-pyruvoyl-tetrahydropterin synthase, ESTs, Weakly similar to JC1405 6-pyruvoyl-tetrahydropterin synthase [H.sapiens], ESTs, Weakly similar to PTPS RAT 6-PYRUVOYL TETRAHYDROBIPTERIN SYNTHASE PRECURSOR [R.norvegicus]	
1727	21882 M83740		l, m	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)		
2693	19694 Z48444		cc, dd	a disintegrin and metalloprotease domain 10, a disintegrin and metalloprotease domain 10	ESTs, Moderately similar to PC4265 disintegrin and metalloproteinase 10 [H.sapiens], Homo sapiens cDNA FLJ13398 fis, clone PLACE1001377, highly similar to Homo sapiens ADAM10 (ADAM10) mRNA, RIKEN cDNA 1700031C13 gene, a disintegrin and metalloprotease domain 10, a disintegrin and metalloproteinase domain 10	

TABLE 3

SEQ. ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2196	22628	NM_024400	kk	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1	ESTs, highly similar to AT5G10050 ADAM-15 & PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2) [M.musculus], ESTs, Weakly similar to AT5G10050 ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1) [M.musculus], ESTs, Weakly similar to T47158 hypothetical protein DKFZp762C110.1 [H.sapiens], Mus musculus, Similar to a disintegrin and metalloprotease with thrombospondin motifs 1 (ADAMTS-1), clone IMAGE:3491991, mRNA, partial cds, Mus musculus, Similar to a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4, clone MGC:38401 IMAGE:5345809, mRNA, complete cds, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 8
2475	19658	NM_057103	gg	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein (gravin) 12, ESTs, Highly similar to gravin [H.sapiens]
2630	2153	U75404	u, v	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein (gravin) 12, ESTs, Highly similar to gravin [H.sapiens]
1930	18956	NM_017075	aa	acetyl-Coenzyme A acetyltransferase 1, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	Homo sapiens, Similar to acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), clone MGC:13582 IMAGE:4278329, mRNA, complete cds, Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), acetyl-Coenzyme A acetyltransferase (peroxisomal 3-oxoacetyl-Coenzyme A thiolase)
1930	18957	NM_017075	r, s, t, ll	acetyl-Coenzyme A acetyltransferase 1, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	Homo sapiens, Similar to acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), clone MGC:13582 IMAGE:4278329, mRNA, complete cds, Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), acetyl-Coenzyme A acetyltransferase (peroxisomal 3-oxoacetyl-Coenzyme A thiolase)
1732	23698	NM_012489	l	acetyl-Coenzyme A acetyltransferase (peroxisomal 3-oxoacetyl-Coenzyme A thiolase)	Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A acetyltransferase (peroxisomal 3-oxoacetyl-Coenzyme A thiolase), acetyl-Coenzyme A acetyltransferase 1 (peroxisomal 3-oxoacetyl-Coenzyme A thiolase)



TABLE 3

SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2037	18569	NM_019212	f, w, x, hh	actin, alpha 1, skeletal muscle	BRG1/brm-associated factor 53A, Rat messenger RNA for alpha-actin, actin, alpha 1, skeletal muscle, actin-like 6, expressed sequence AA959943
275	16001	AA866452	bb, cc, dd	actin, alpha, cardiac, actin, alpha, cardiac muscle	ESTs, Weakly similar to ACTA_HUMAN Actin, aortic smooth muscle (Alpha-actin 2) [R.norvegicus], Homo sapiens, clone MGC:33407 IMAGE:4824606, mRNA, complete cds, actin, alpha 2, smooth muscle, aorta, smooth muscle alpha-actin
2212	21166	NM_031005	a, n, o	actinin, alpha 1	ESTs, Weakly similar to alpha actinin 4 [Mus musculus] [M.musculus], RIKEN cDNA 3110023F10 gene, actinin alpha 2, actinin alpha 3, actinin, alpha 1, actinin, alpha 2, actinin, alpha 3, alpha actinin 4
2307	5358	NM_031675	r	actinin, alpha 4, alpha actinin 4	ESTs, Weakly similar to alpha actinin 4 [Mus musculus] [M.musculus], RIKEN cDNA 3110023F10 gene, actinin, alpha 4, alpha actinin 4
1821	24431	NM_012912	a, p, q, y, z, ee, ff	activating transcription factor 3	ESTs, Weakly similar to A39382 liver regeneration factor LRF1 - rat [R.norvegicus], ESTs, Weakly similar to A54025 transcription factor ATF3 [H.sapiens], activating transcription factor 3
1864	20242	NM_013084	gg	acyl-Coenzyme A dehydrogenase, short/branched chain	acyl-Coenzyme A dehydrogenase, short/branched chain
903	17957	A1028975	s, t	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 1, beta 1 subunit	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 1, beta 1 subunit
1990	17959	NM_017277	s, t	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 1, beta 1 subunit	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 1, beta 1 subunit
2495	17958	NM_080583	gg	adaptor-related protein complex 2, beta 1 subunit	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 2, beta 1 subunit
2495	17960	NM_080583	r	adaptor-related protein complex 2, beta 1 subunit	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 2, beta 1 subunit
2366	1596	NM_053294	r	adenosine A2a receptor	adenosine A2a receptor, adenosine A3 receptor
1816	16708	NM_012895	u, v	adenosine kinase	adenosine kinase, expressed sequence A1987814
2053	8200	NM_019285	ll	adenylate cyclase 4	ESTs, Moderately similar to A41542 adenylate cyclase (EC 4.6.1.1) IV - rat [R.norvegicus], adenylate cyclase 2 (brain), adenylate cyclase 4
2521	24775	NM_133511	c	adenylate cyclase activating polypeptide 1 (pituitary) receptor type 1, adenylate cyclase activating polypeptide 1 receptor 1	ESTs, Weakly similar to PACR MOUSE PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE I RECEPTOR PRECURSOR [M.musculus], adenylate cyclase activating polypeptide 1 (pituitary) receptor type I, adenylate cyclase activating polypeptide 1 receptor 1
1905	17972	NM_016989	l, m	adenylate cyclase activating polypeptide 1, adenylate cyclase activating polypeptide 1 (pituitary)	adenylate cyclase activating polypeptide 1, adenylate cyclase activating polypeptide 1 (pituitary)

TABLE 3

SEQ ID		GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atfy, Ref. 44921-5090-01-WO/2105485
						ESTs, Highly similar to 191/150A collagen:SUBUNIT1=alpha1:ISO1TYPE=VIII [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to CA18 MOUSE COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to ACR3 MOUSE 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR [M.musculus], Mus musculus, Similar to DKFZP586B0621 protein, clone MGC:38635 IMAGE:5355789, mRNA, complete cds, RIKEN cDNA 5530401N20 gene, adipose most abundant gene transcript 1, collagen, type VIII, alpha 1, procollagen, type VIII, alpha 1	
2577		13712	NM_144744	ii	adipose most abundant gene transcript 1	ADP-ribosylarginine hydrolase, ESTs, Weakly similar to ADP-RIBOSYLARGININE HYDROLASE [M.musculus]	
1728		3762	M86341	s, t	ADP-ribosylarginine hydrolase	ADP-ribosylation factor 4-like, ADP-ribosylation factor-like 7, ADP-ribosylation-like 4, ESTs, Weakly similar to ADP-ribosylation-like 4 [Mus musculus] [M.musculus], Mus musculus, Similar to ADP-ribosylation-like 4, clone MGC:5774 IMAGE:3599701, mRNA, complete cds, RIKEN cDNA 1110036H21 gene, epithelial protein lost in neoplasm beta	
2032		24019	NM_019186	j, k	ADP-ribosylation factor-like 4, ADP-ribosylation-like 4	ESTs, Weakly similar to GRK6 MOUSE G PROTEIN-COUPLED RECEPTOR KINASE GRK6 [M.musculus], G protein-coupled receptor kinase 6, adrenergic receptor kinase, beta 1, adrenergic, beta, receptor kinase 1	
735		3505	AA998430	w, x	adrenergic receptor kinase 1	adrenomedullin	
1906		64	NM_016991	jj, kk	adrenergic receptor, alpha 1b, adrenergic, alpha-1B-, receptor		
1778		322	NM_012715	d, gg	adrenomedullin		
						ESTs, Weakly similar to A38096 perlecan precursor [H.sapiens], ESTs, Weakly similar to AGRT agrin - rat [R.norvegicus], ESTs, Weakly similar to BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR [M.musculus], ESTs, Weakly similar to PGBM_HUMAN BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR [H.sapiens], Mus musculus, clone IMAGE:3494258, mRNA, partial cds, heparan sulfate proteoglycan 2 (perlecan), perlecan (heparan sulfate proteoglycan 2), serine protease inhibitor, Kazal type, 5, sialoadhesin, transmembrane protein with EGF-like and two follistatin-like domains 1	
1725		10743	M64780	r, jj, kk	agrin		

TABLE 3

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atty. Ref. 44921-5090-01-WO/2105485
1725	10744	M64780	f	agrin	ESTs, Weakly similar to A38096 perlecan precursor [H.sapiens], ESTs, Weakly similar to AGRT agrin - rat [R.norvegicus], ESTs, Weakly similar to BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR [M.musculus], ESTs, Weakly similar to PGBM_HUMAN BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR [H.sapiens], Mus musculus, clone IMAGE:3494258, mRNA, partial cds, heparan sulfate proteoglycan 2 (perlecan), perlecan (heparan sulfate proteoglycan 2), serine protease inhibitor, Kazal type, 5, sialoadhesin, transmembrane protein with EGF-like and two follistatin-like domains 1	
2082	23424	NM_021680	j, k	alanyl-tRNA synthetase	alanyl-tRNA synthetase	
2118	20915	NM_022407	kk	aldehyde dehydrogenase 1 family, member A1, aldehyde dehydrogenase family 1, subfamily A1	Mus musculus, Similar to aldehyde dehydrogenase 8 family, member A1, clone IMAGE:4234742, mRNA, partial cds, aldehyde dehydrogenase 1 family, member A1, aldehyde dehydrogenase family 1, subfamily A1	
2353	12299	NM_032416	c	aldehyde dehydrogenase 2 family (mitochondrial), aldehyde dehydrogenase 2, mitochondrial	ESTs, Moderately similar to DHAM_RAT ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (ALDH CLASS 2) (ALDH1) (ALDH-E2) [R.norvegicus], RIKEN cDNA 2410004H02 gene, aldehyde dehydrogenase 1 family, member B1, aldehyde dehydrogenase 2 family (mitochondrial), aldehyde dehydrogenase 2, mitochondrial	
119	11901	AA801058	d	aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1	Mus musculus, Similar to aldehyde dehydrogenase 4 family, member A1, clone IMAGE:5102023, mRNA, partial cds, RIKEN cDNA 1110038I05 gene, aldehyde dehydrogenase 4 family, member A1, aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1	
1733	15511	NM_012498	ii	aldo-keto reductase family 1, member B1 (aldose reductase), aldo-keto reductase family 1, member B3 (aldose reductase)	EST, Weakly similar to A39763 aldehyde reductase [H.sapiens], ESTs, Moderately similar to ALDR_RAT Aldose reductase (AR) (Aldehyde reductase) [R.norvegicus], ESTs, Weakly similar to ALDR_RAT Aldose reductase (AR) (Aldehyde reductase) [R.norvegicus], Rattus norvegicus mRNA for aldose reductase-like protein, aldo-keto reductase family 1, member B1 (aldose reductase), aldo-keto reductase family 1, member B3 (aldose reductase)	
1802	15032	NM_012816	j, k, jj, kk	alpha-methylacyl-CoA racemase	alpha-methylacyl-CoA racemase, cDNA sequence AF397014, chromosome 7 open reading frame 10	
2039	2079	NM_019220	c	amino-terminal enhancer of split	amino-terminal enhancer of split	

TABLE 3						Atly. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
				amyloid beta (A4) precursor protein-binding, family B, member 1, amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	Mus musculus, Similar to amyloid beta (A4) precursor protein-binding, family B, member 3, clone MGC:38710 IMAGE:5357681, mRNA, complete cds, amyloid beta (A4) precursor protein-binding, family B, member 1, amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65), amyloid beta (A4) precursor protein-binding, family B, member 2	
2663	25711	X60468	s, t		ESTs, Highly similar to A31759 peptidyl-dipeptidase A [H.sapiens], RIKEN cDNA 2010305L05 gene, angiotensin I converting enzyme (peptidyl-dipeptidase A) 1, angiotensin converting enzyme	
1745	225	NM_012544	aa, bb	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1, angiotensin converting enzyme	annexin A1	
1818	7196	NM_012904	a, ll	annexin A1	annexin A2, annexin A9	
1366	15315	AI177911	h, l	annexin A2	EST, Moderately similar to U806162C protein COI [M.musculus], EST, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], EST, Weakly similar to 0806162C protein COI [M.musculus], ESTs, Highly similar to hydroxyacid oxidase 3 (medium-chain) [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], ESTs, Weakly similar to 0806162C protein COI [M.musculus], annexin A2, annexin A9, hydroxyacid oxidase (glycolate oxidase) 3, hydroxyacid oxidase 1, liver	
2073	574	NM_019905	a, h, l, z, aa, kk, ll	annexin A2, hydroxyacid oxidase (glycolate oxidase) 3, hydroxyacid oxidase 3 (medium-chain)	ESTs, Moderately similar to ANX4 MOUSE ANNEXIN IV [M.musculus], ESTs, Weakly similar to ZAP 36/annexin IV [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to annexin A8, clone MGC:13875 IMAGE:4013266, mRNA, complete cds, annexin A13, annexin A4, annexin A8	
1559	8440	AI235611	b	annexin A4	annexin A6	
2181	561	NM_024156	jj, kk	annexin A6	annexin A6	
2181	562	NM_024156	r	annexin A6	ESTs, Moderately similar to AOP2 MOUSE ANTIOXIDANT PROTEIN 2 [M.musculus], ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 [H.sapiens], anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5	
2398	19252	NM_053576	a	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5	aortic preferentially expressed gene 1, nuclear protein, marker for differentiated aortic smooth muscle and down-regulated with vascular injury	
				aortic preferentially expressed gene 1, nuclear protein, marker for differentiated aortic smooth muscle and down-regulated with vascular injury	APEX nuclease (multifunctional DNA repair enzyme), Mus musculus ape2 mRNA for AP endonuclease 2, complete cds, apurinic/apurimidinic endonuclease	
1819	1834	NM_012905	d	APEX nuclease (multifunctional DNA repair enzyme), apurinic/apurimidinic endonuclease		
2177	20801	NM_024148	d, s, t			

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SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2552	16400	NM_138828	cc, dd	apolipoprotein E	apolipoprotein E	
1793	5758	NM_012778	p, q, s, t	aquaporin 1, aquaporin 1 (channel-forming integral protein, 28kD)	aquaporin 1, aquaporin 1 (channel-forming integral protein, 28kD)	
1794	104	NM_012779	ii	aquaporin 5	aquaporin 5, aquaporin 6	
1986	7593	NM_017260	w, x	arachidonate 5-lipoxygenase activating protein, arachidonate 5-lipoxygenase-activating protein	arachidonate 5-lipoxygenase activating protein, arachidonate 5-lipoxygenase-activating protein	
1986	7594	NM_017260	w, x, ii	arachidonate 5-lipoxygenase activating protein, arachidonate 5-lipoxygenase-activating protein	arachidonate 5-lipoxygenase activating protein, arachidonate 5-lipoxygenase-activating protein	
1907	24868	NM_016992	n, o	arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal)	arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal)	
1907	24869	NM_016992	n, o	arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal)	arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal)	
				ARP3 actin-related protein 3 homolog (yeast), EST, Weakly similar to ARP3_HUMAN ACTIN-LIKE PROTEIN 3 [H.sapiens], EST, Weakly similar to actin, skeletal muscle - rat [R.norvegicus], ESTs, Moderately similar to ARP3_HUMAN ACTIN-LIKE PROTEIN 3 [H.sapiens], ESTs, Weakly similar to ATHU actin alpha 1, skeletal muscle [H.sapiens], Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955, actin-related protein 3-beta, hypothetical protein FLJ12785, mitochondrial ribosomal protein L47		
1464	23013	A1230743	hh	ARP3 actin-related protein 3 homolog (yeast), actin-related protein 3 homolog (yeast)	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1, ESTs, Highly similar to AT91_HUMAN ATP SYNTHASE LIPID-BINDING PROTEIN P1 PRECURSOR [H.sapiens], Homo sapiens cDNA: FLJ23586 fis, clone LNG14376	
2000	16844	NM_017311	n, o	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit, RIKEN cDNA 2410043G19 gene, expressed sequence AV000645	
2566	17203	NM_139099	g, hh	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit, RIKEN cDNA 2410043G19 gene, expressed sequence AV000645	
2566	17204	NM_139099	g	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit		
1994	12347	NM_017290	ll	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2		
1994	12349	NM_017290	aa	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2		

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1731	17991	M96626	cc, dd, gg	ATPase, Ca++ transporting, plasma membrane 3	ATPase, Ca++ transporting, plasma membrane 2, ATPase, Class V, type 10C, ATPase, class V, type 10A, ESTs, Highly similar to A34308 Ca2+-transporting ATPase [R.norvegicus], ESTs, Weakly similar to I49143 gastric H(+)-K(+)-ATPase alpha subunit - mouse [M.musculus], RIKEN cDNA 111001914 gene, RIKEN cDNA 2810442/22 gene	
1822	24783	NM_012914	kk	ATPase, Ca++ transporting, ubiquitous	ATPase, Ca++ transporting, ubiquitous	
1734	583	NM_012505	h, l	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide, ATPase, Na+/K+ transporting, alpha 2 polypeptide	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide, ATPase, Na+/K+ transporting, alpha 4 polypeptide, ESTs, Highly similar to A1A4_HUMAN Sodium/potassium-transporting ATPase alpha-4 chain (Sodium pump 4) (Na+/K+ ATPase 4) [H.sapiens], expressed sequence AW060654	
1726	5733	M81855	d	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	ATP-binding cassette, sub-family B (MDR/TAP), member 1, ATP-binding cassette, sub-family B (MDR/TAP), member 1A, ATP-binding cassette, sub-family B (MDR/TAP), member 1B, EST, Highly similar to MDR3 MOUSE MULTIDRUG RESISTANCE PROTEIN 3 [M.musculus], EST, Weakly similar to MULTIDRUG RESISTANCE PROTEIN 3 [M.musculus], ESTs, Weakly similar to MDR1 MOUSE MULTIDRUG RESISTANCE PROTEIN 1 [M.musculus], Mus musculus, clone IMAGE:3588242, mRNA, partial cds	
2656	1037	X57523	d	ATP-binding cassette, sub-family B (MDR/TAP), member 2, transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	ATP-binding cassette, sub-family B (MDR/TAP), member 2, ESTs, Highly similar to S13426 multidrug resistance protein homolog - rat [R.norvegicus], transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	
1853	733	NM_013040	j, k	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9, ESTs, Weakly similar to T42751 sulfonyleurea receptor 2 - rat [R.norvegicus], Homo sapiens cDNA FLJ31957 fis, clone NT2RP7007381, highly similar to Sulfonyleurea receptor 2A, Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330439B14:ATP-binding cassette, sub-family C (CFTR/MRP), member 9, full insert sequence	
728	3511	AA998152	ee, ff	BAI1-associated protein 2, brain-specific angiogenesis inhibitor 1-associated protein 2	BAI1-associated protein 2, ESTs, Weakly similar to brain-specific angiogenesis inhibitor 1-associated protein 2 [Mus musculus] [M.musculus], Mus musculus, Similar to KIAA0429 gene product, clone IMAGE:2811240, mRNA, partial cds, RIKEN cDNA 1300006M19 gene, brain-specific angiogenesis inhibitor 1-associated protein 2, hypothetical protein FLJ22582, insulin receptor tyrosine kinase substrate	

TABLE 3

SEQ ID	GenBank Acc. GLGC ID No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2370	1063 NM_053328	e	basic helix-loop-helix domain containing, class B, 2, basic helix-loop-helix domain containing, class B2	basic helix-loop-helix domain containing, class B, 2, basic helix-loop-helix domain containing, class B, 3, basic helix-loop-helix domain containing, class B2, basic helix-loop-helix domain containing, class B3
2514	1061 NM_133303	p, q, hh	basic helix-loop-helix domain containing, class B3	basic helix-loop-helix domain containing, class B, 2, basic helix-loop-helix domain containing, class B2, basic helix-loop-helix domain containing, class B3
1984	19 NM_017258	p, q	B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative, Homo sapiens cDNA FLJ30547 f1s, clone BRAWH2001439, transducer of ERBB2, 1, transducer of ERBB2, 2, transducer of ErbB-2.1
1985	15300 NM_017259	p, q, kk	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]
1985	15301 NM_017259	j, k, p, q, y, z, gg	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]
1985	15299 NM_017259	y, z	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]
1924	910 NM_017059	d	BCL2-associated X protein, Bcl2-associated X protein	
1924	911 NM_017059	d	BCL2-associated X protein, Bcl2-associated X protein	
1924	912 NM_017059	d, l, m	BCL2-associated X protein, Bcl2-associated X protein	
1913	17815 NM_017015	w, x	beta-glucuronidase, glucuronidase, beta	ESTs, Highly similar to A26581 beta-glucuronidase [H.sapiens], SMA3, beta-glucuronidase structural, glucuronidase, beta
1933	22552 NM_017087	n, o	biglycan	ESTs, Highly similar to asporin (LRR class 1); periodontal ligament associated protein 1 [Homo sapiens] [H.sapiens], ESTs, Weakly similar to PGS1_RAT Bone/cartilage proteoglycan I precursor (Biglycan) (PG-S1) [R.norvegicus], asporin, biglycan
1735	1745 NM_012513	p, q, ll	brain derived neurotrophic factor, brain-derived neurotrophic factor	brain derived neurotrophic factor, brain-derived neurotrophic factor, expressed sequence A1462899
495	23038 AA900881	a, j, k, y, z	branched chain aminotransferase 1, cytosolic	branched chain aminotransferase 1, cytosolic
2117	24643 NM_022400	b, u, v	branched chain aminotransferase 2, mitochondrial	Homo sapiens cDNA FLJ13847 f1s, clone THYRO1000852, highly similar to Human branched-chain amino acid aminotransferase (ECA40) mRNA, branched chain aminotransferase 2, mitochondrial

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1688	17285	J02827	c	branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease), branched chain ketoacid dehydrogenase E1, alpha polypeptide		
778	3278	A1008988	y, z	breakpoint cluster region		ESTs, Highly similar to breakpoint cluster region, isoform 1 [Homo sapiens] [H.sapiens], ESTs, Highly similar to chimerin (chimaerin) 1 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to SH3-BINDING PROTEIN 3BP-1 [M.musculus], RIKEN cDNA 1700112L09 gene, RIKEN cDNA 2310069I04 gene, RIKEN cDNA 5133400C09 gene, RIKEN cDNA 5730403H17 gene, SH3-domain binding protein 1, breakpoint cluster region, chimerin (chimaerin) 1
2347	18499	NM_031984	aa, bb	calbindin 1, (28kD), calbindin-28K		Mus musculus, Similar to secretagogin, clone MGC:27615 IMAGE:4504330, mRNA, complete cds, calbindin 1, (28kD), calbindin-28K
2347	18500	NM_031984	bb	calbindin 1, (28kD), calbindin-28K		Mus musculus, Similar to secretagogin, clone MGC:27615 IMAGE:4504330, mRNA, complete cds, calbindin 1, (28kD), calbindin-28K
1780	1632	NM_012717	u, v	calcitonin receptor-like		calcitonin receptor-like
						ESTs, Highly similar to CIC2 RAT DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2DELTA SUBUNITS PRECURSOR [R.norvegicus], ESTs, Moderately similar to CIC2 RAT DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2DELTA SUBUNITS PRECURSOR [R.norvegicus], Rattus norvegicus L-type calcium channel alpha2/delta subunit mRNA, complete cds, calcium channel, voltage-dependent, alpha 2/delta subunit 1, calcium channel, voltage-dependent, alpha 2/delta subunit 2, calcium channel, voltage-dependent, alpha2/delta subunit 1
1824	1765	NM_012919	u, v	calcium channel, voltage-dependent, alpha 2/delta subunit 1, calcium channel, voltage-dependent, alpha2/delta subunit 1		ESTs, Weakly similar to 211412A Ca channel:SUBUNIT=beta [M.musculus], calcium channel, voltage-dependent, beta 2 subunit, expressed sequence AW060387
2442	1011	NM_053851	e	calcium channel, voltage-dependent, beta 2 subunit		RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence A1327027, expressed sequence AL024000, troponin C, fast skeletal
2340	19190	NM_031969	h, i	calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)		RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence A1327027, expressed sequence AL024000, troponin C, fast skeletal
2340	19191	NM_031969	h, i	calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)		RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence A1327027, expressed sequence AL024000, troponin C, fast skeletal



TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2340	19195	NM_031969	h, l, ll	calmodulin 1 (phosphorylase kinase, delta)	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence A1327027, expressed sequence AL024000, troponin C, fast skeletal	
2340	25802	NM_031969	h, l, aa, bb, ll	calmodulin 1 (phosphorylase kinase, delta)	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence A1327027, expressed sequence AL024000, troponin C, fast skeletal	
587	15476	AA944426	h, l	calmodulin 3 (phosphorylase kinase, delta)	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence A1327027, expressed sequence AL024000, troponin C, fast skeletal	
1736	20518	NM_012518	n, o, r	calmodulin 3 (phosphorylase kinase, delta)	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence A1327027, expressed sequence AL024000, troponin C, fast skeletal	
1698	6963	L18889	e	calhexin		
2024	20863	NM_019152	cc, dd	calpain 1, calpain 1, (mu/l) large subunit	ESTs, Weakly similar to CAN1_MOUSE CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE) [M.musculus], calpain 1, calpain 11, small optic lobes homolog (Drosophila) [M.musculus], calpain 1, calpain 11, small optic lobes homolog (Drosophila) [M.musculus], Moderately similar to ICAL_HUMAN CALPAIN INHIBITOR [H.sapiens], calpastatin	
296	1190	AA875089	hh	calpastatin	ESTs, Moderately similar to CALPONIN H1, SMOOTH MUSCLE [M.musculus], calponin 1, calponin 2, calponin 3, acidic	
2064	23491	NM_019359	r	calponin 3, acidic	ESTs, Highly similar to CAQS MOUSE CALSEQUESTIN, SKELETAL MUSCLE [SOFORM PRECURSOR [M.musculus], ESTs, Moderately similar to CAQC_RAT CALSEQUESTIN, CARDIAC MUSCLE ISOFORM PRECURSOR [R.norvegicus], calsequestrin 1, calsequestrin 1 (fast-twitch, skeletal muscle), calsequestrin 2, calsequestrin 2 (cardiac muscle)	
530	168	AA924985	e	calsequestrin 2, calsequestrin 2 (cardiac muscle)		

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1946		167 NM_017131	b, e, u, v, ll	calsequestin 2, calsequestin 2 (cardiac muscle)	ESTs, Highly similar to CAQS MOUSE CALSEQUESTIN, SKELETAL MUSCLE ISOFORM PRECURSOR [M.musculus], ESTs, Moderately similar to CAQC, RAT CALSEQUESTIN, CARDIAC MUSCLE ISOFORM PRECURSOR [R.norvegicus], calsequestin 1, calsequestin 1 (fast-twitch, skeletal muscle), calsequestin 2, calsequestin 2 (cardiac muscle)	
					EST, Weakly similar to CRMS2 carbonate dehydratase [M.musculus], ESTs, Weakly similar to CAH2_RAT Carbonic anhydrase II (Carbonate dehydratase II) (CA-II) [R.norvegicus], carbonic anhydrase 2, carbonic anhydrase I, carbonic anhydrase II, carbonic anhydrase VIII, carbonic anhydrase-like sequence 1	
2056		15056 NM_019291	b, c	carbonic anhydrase 2, carbonic anhydrase II	ESTs, Weakly similar to S52349 carbonyl reductase (NADPH) (EC 1.1.1.184) - rat [R.norvegicus], RIKEN cDNA 1110001J05 gene, RIKEN cDNA A930033N07 gene, carbonyl reductase 1, carbonyl reductase 3	
2029		17063 NM_019170	f, g	carbonyl reductase 1	ESTs, Weakly similar to S52349 carbonyl reductase (NADPH) (EC 1.1.1.184) - rat [R.norvegicus], RIKEN cDNA 1110001J05 gene, RIKEN cDNA A930033N07 gene, carbonyl reductase 1, carbonyl reductase 3	
2029		17064 NM_019170	f, g	carbonyl reductase 1	ESTs, Weakly similar to S52349 carbonyl reductase (NADPH) (EC 1.1.1.184) - rat [R.norvegicus], RIKEN cDNA 1110001J05 gene, RIKEN cDNA A930033N07 gene, carbonyl reductase 1, carbonyl reductase 3	
2029		17066 NM_019170	g	carbonyl reductase 1	ESTs, Weakly similar to A41010 carboxylesterase [H.sapiens], Mus musculus, Similar to carboxylesterase 2 (intestine, liver), clone MGC:18908 IMAGE:4241028, mRNA, complete cds, Mus musculus, clone MGC:18894 IMAGE:4239756, mRNA, complete cds, RIKEN cDNA 2310039D24 gene, T-complex expressed gene 5, carboxylesterase 1, carboxylesterase 1 (monocyte/macrophage serine esterase 1), carboxylesterase 3, carboxylesterase 3 (brain), carboxylesterase-related protein, esterase 22	
2512		20879 NM_133295	hh	carboxylesterase 3, carboxylesterase 3 (brain)	EST, Weakly similar to MAST CELL CARBOXYPEPTIDASE A PRECURSOR [M.musculus], RIKEN cDNA 1110019K20 gene, RIKEN cDNA 4930430M09 gene, carboxypeptidase A1 (pancreatic), carboxypeptidase B1 (tissue)	
1908		24354 NM_016998	c	carboxypeptidase A1, carboxypeptidase A1 (pancreatic)		
1875		21840 NM_013128	w, ll	carboxypeptidase E		
2350		20554 NM_031987	b, l, m, aa, cc, dd	carnitine O-octanoyltransferase	carnitine O-octanoyltransferase	
2350		20555 NM_031987	j, k	carnitine O-octanoyltransferase	carnitine O-octanoyltransferase	

TABLE 3				Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1896	20855	NM_013200	a, w, x, hh	caritine palmitoyltransferase 1, muscle, caritine	caritine palmitoyltransferase 1, muscle, caritine palmitoyltransferase I, muscle
1896	20856	NM_013200	a, w, x, aa, hh, ll	palmitoyltransferase I, muscle	
1827	1977	NM_012930	a, w, x, cc, dd	caritine palmitoyltransferase 2, caritine	
2409	20243	NM_053615	aa, bb	casein kinase 1, alpha 1	caritine palmitoyltransferase II
630	22771	AA946432	b, l, m	casein kinase 1, delta	ESTs, Weakly similar to casein kinase [M.musculus], RIKEN cDNA 2610208K14 gene, RIKEN cDNA 3300002K07 gene, casein kinase 1, alpha 1, delta
1738	15741	NM_012520	ll	catalase, catalase 1	ESTs, Moderately similar to KC1D_HUMAN CASEIN KINASE I, DELTA ISOFORM [H.sapiens], ESTs, Weakly similar to casein kinase [M.musculus], RIKEN cDNA 2610208K14 gene, RIKEN cDNA 3300002K07 gene, casein kinase 1, alpha 1, delta
1740	11115	NM_012531	f, g	catechol-O-methyltransferase	casein kinase 1, delta
1740	11116	NM_012531	f, g	catechol-O-methyltransferase	catalase, catalase 1
1937	2150	NM_017097	a, ll	cathepsin C	RIKEN cDNA 6330414C15 gene, catechol-O-methyltransferase
1882	3430	NM_013156	c, l, m, t, kk	cathepsin L	RIKEN cDNA 6330414C15 gene, catechol-O-methyltransferase
1882	3431	NM_013156	c, kk	cathepsin L	RIKEN cDNA 492153717 gene, cathepsin C
2284	25795	NM_031556	jj, kk	caveolin 1, caveolae protein, 22kD, caveolin protein, 22 kDa	ESTs, Weakly similar to CATL MOUSE CATHEPSIN L PRECURSOR [M.musculus], RIKEN cDNA 4930486L24 gene, cathepsin L, expressed sequence AA408230
2172	21238	NM_024125	p, q	CCAAT/enhancer binding protein (C/EBP), beta	ESTs, Weakly similar to CATL MOUSE CATHEPSIN L PRECURSOR [M.musculus], RIKEN cDNA 4930486L24 gene, cathepsin L, expressed sequence AA408230
2172	21239	NM_024125	p, q, r, bb, ee, ff, kk	CCAAT/enhancer binding protein (C/EBP), beta	caveolin 1, caveolae protein, 22kD, caveolin, caveolae protein, 22 kDa
1880	21682	NM_013154	j, k, p, q, y, z, gg, kk	CCAAT/enhancer binding protein (C/EBP), delta	CCAAT/enhancer binding protein (C/EBP), beta
1880	21683	NM_013154	e, j, k, p, q, y, z, kk	CCAAT/enhancer binding protein (C/EBP), delta	CCAAT/enhancer binding protein (C/EBP), beta

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2280	16049	NM_031541	n, o	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1, scavenger receptor class B1	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1, scavenger receptor class B1	
2286	18315	NM_031561	e, u	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	
2286	18316	NM_031561	e	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	
2286	18317	NM_031561	r, aa, bb, ii	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	
2286	18319	NM_031561	w, x	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	
1874	2005	NM_013127	e, bb	CD38 antigen, CD38 antigen (p45)	CD38 antigen, CD38 antigen (p45)	
1826	1625	NM_012924	gg	CD44 antigen, CD44 antigen (homing function and Indian blood group system)		
386	2832	AA892388	b, u, v	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344), CD59a antigen		
1943	1435	NM_017125	kk	CD63 antigen (melanoma 1 antigen), Cd63 antigen	CD63 antigen (melanoma 1 antigen), Cd63 antigen, EST, Weakly similar to CD63 MOUSE CD63 ANTIGEN [M.musculus], ESTs, Weakly similar to CD63_RAT CD63 antigen (AD1 antigen) [R.norvegicus], Mus musculus, clone MGC:36554 IMAGE:4954874, mRNA, complete cds, RIKEN cDNA 1300010A20 gene, expressed sequence C75951, expressed sequence C80071, transmembrane 4 superfamily member 2	
2424	10510	NM_053743	u, v	CDC37 cell division cycle 37 homolog (S. cerevisiae), cell division cycle 37 homolog (S. cerevisiae)	CDC37 cell division cycle 37 homolog (S. cerevisiae), cell division cycle 37 homolog (S. cerevisiae)-like	
73	13683	AA799788	e	cell division cycle 34	ESTs, Highly similar to A41222 ubiquitin-protein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus], RIKEN cDNA 2610301N02 gene, cell division cycle 34, expressed sequence A1327276, ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae), ubiquitin-conjugating enzyme E2C	

TABLE 3					
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1702	13682138482		e	cell division cycle 34	ESTs, Highly similar to A41222 ubiquitin-protein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus], RIKEN cDNA 2610301N02 gene, cell division cycle 34, expressed sequence A1327276, ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae), ubiquitin-conjugating enzyme E2C
1423	22845A1227887		e, aa, bb	cell division cycle 42 (GTP binding protein, 25kD), cell division cycle 42 homolog (S. cerevisiae)	RIKEN cDNA 4930544G11 gene, RIKEN cDNA 5830400A04 gene, cell division cycle 42 (GTP binding protein, 25kD), plasia ras-related homolog A2, ras homolog 9 (RhoC), ras homolog A2, ras homolog gene family, member C
1741	16520NM_012532		c	ceruloplasmin, ceruloplasmin (ferroxidase)	DNA segment, Chr 3, ERATO Doi 555, expressed EST, Highly similar to FA8_HUMAN COAGULATION FACTOR VIII PRECURSOR [H.sapiens], ESTs, Weakly similar to CERU_MOUSE CERULOPLASMIN PRECURSOR [M.musculus], ESTs, Weakly similar to CERU_RAT CERULOPLASMIN PRECURSOR (FERROXIDASE) [R.norvegicus], ESTs, Weakly similar to KUHU ferroxidase [H.sapiens], ceruloplasmin, ceruloplasmin (ferroxidase), coagulation factor VIII, procoagulant component (hemophilia A)
2321	19048NM_031719		jj, kk	chloride channel, nucleotide-sensitive, 1A	chloride channel, nucleotide-sensitive, 1A
2329	1182NM_031790		b, l, m	citron, citron (rho-interacting, serine/threonine kinase 21)	EST, Highly similar to CTRO_HUMAN CITRON PROTEIN [H.sapiens], ESTs, Highly similar to CTRO_HUMAN CITRON PROTEIN [H.sapiens], KIAA0451 gene product, Nef-associated factor 1, citron, citron (rho-interacting, serine/threonine kinase 21)
2344	17075NM_031974		gg	clathrin, light polypeptide (Lca)	H.sapiens clathrin light chain a gene, clathrin, light polypeptide (Lca), clathrin, light polypeptide (Lcb), expressed sequence AV026556
216	13627AA851493		aa, bb	claudin 7	ESTs, Weakly similar to CLD7_RAT CLAUDIN-7 [R.norvegicus], Mus musculus claudin 19 mRNA, complete cds, claudin 10, claudin 15, claudin 7
1952	15364NM_017147		ii	cofilin 1 (non-muscle), cofilin 1, non-muscle	cofilin 1 (non-muscle), cofilin 1, non-muscle, cofilin 2 (muscle), cofilin 2, muscle, expressed sequence AW987265
1952	15365NM_017147		aa, bb, ll	cofilin 1 (non-muscle), cofilin 1, non-muscle	cofilin 1 (non-muscle), cofilin 1, non-muscle, cofilin 2 (muscle), cofilin 2, muscle, expressed sequence AW987265
1659	16610D28557		c, f, u, v	cold shock domain protein A	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:261020519:Y box protein 1, full insert sequence, Mus musculus Y-box binding protein (oxyR) mRNA, partial cds, cold shock domain protein A

TABLE 3					Attv. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1485	15572	A1231472	f, g	collagen, type I, alpha 1	EST, Weakly similar to CAT1_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], F-box only protein 29, Mus musculus, Similar to RIKEN cDNA 1700051112 gene, clone MGC:28741 IMAGE:4481590, mRNA, complete cds, collagen, type IV, alpha 3 (Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha 1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV, alpha 5, procollagen, type VI, alpha 1, putative emu1 EST, Weakly similar to CAT1_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], F-box only protein 29, Mus musculus, Similar to RIKEN cDNA 1700051112 gene, clone MGC:28741 IMAGE:4481590, mRNA, complete cds, collagen, type IV, alpha 3 (Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha 1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV, alpha 5, procollagen, type VI, alpha 1, putative emu1
1713	15571	M27207	g	collagen, type I, alpha 1	EST, Weakly similar to CAT1_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], F-box only protein 29, Mus musculus, Similar to RIKEN cDNA 1700051112 gene, clone MGC:28741 IMAGE:4481590, mRNA, complete cds, collagen, type IV, alpha 3 (Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha 1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV, alpha 5, procollagen, type VI, alpha 1, putative emu1 EST, Weakly similar to CAT1_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], F-box only protein 29, Mus musculus, Similar to RIKEN cDNA 1700051112 gene, clone MGC:28741 IMAGE:4481590, mRNA, complete cds, collagen, type IV, alpha 3 (Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha 1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV, alpha 5, procollagen, type VI, alpha 1, putative emu1
2696	15569	Z78279	c, g, bb	collagen, type I, alpha 1	EST, Weakly similar to CAT1_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], F-box only protein 29, Mus musculus, Similar to RIKEN cDNA 1700051112 gene, clone MGC:28741 IMAGE:4481590, mRNA, complete cds, collagen, type IV, alpha 3 (Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha 1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV, alpha 5, procollagen, type VI, alpha 1, putative emu1

TABLE 3					Atty. Ref. 44921-5090-01-WO/2106485	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2696	15570	Z78279	c, f, g, j, k	collagen, type I, alpha 1, procollagen, type I, alpha 1	EST, weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], F-box only protein 29, Mus musculus, Similar to RIKEN cDNA 1700051112 gene, clone MGC:28741 IMAGE:4481590, mRNA, complete cds, collagen, type IV, alpha 3 (Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha 1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 5, procollagen, type IV, alpha 1, putative emu1	
2	6153	AA875531	g, j, k	collagen, type I, alpha 2, procollagen, type I, alpha 2	EST, Moderately similar to 0806162B cytochrome b [M.musculus], EST, Moderately similar to 810024B cytochrome b [H.sapiens], EST, Weakly similar to 0806162B cytochrome b [M.musculus], EST, Weakly similar to 0812187A cytochrome b [Rattus norvegicus] [R.norvegicus], EST, Weakly similar to 810024M URF 6 [H.sapiens], F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	
233	6158	AA859284	f, g	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	
2376	6154	NM_053356	f, g	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	
2376	6155	NM_053356	g	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	
2376	6156	NM_053356	g	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	
2376	6157	NM_053356	f, g	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	

TABLE 3

SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atty. Ref. 44921-5090-01-WO/2105485
1711	16427	M21354	f, g	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1	EST, Highly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Moderately similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to CA13 MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus], EST, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to S41067 collagen alpha 1(III) chain - rat [R.norvegicus], Mus musculus, Similar to putative protein phosphatase 1 nuclear targeting subunit, clone IMAGE:3157989, mRNA, partial cds, RIKEN cDNA 2010011D20 gene, cleavage and polyadenylation specific factor 6, 68kD subunit, collagen type V, alpha 2, collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1	
2674	16426	X70369	c, g, bb	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1	EST, Highly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Moderately similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to CA13 MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus], EST, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to S41067 collagen alpha 1(III) chain - rat [R.norvegicus], Mus musculus, Similar to putative protein phosphatase 1 nuclear targeting subunit, clone IMAGE:3157989, mRNA, partial cds, RIKEN cDNA 2010011D20 gene, cleavage and polyadenylation specific factor 6, 68kD subunit, collagen type V, alpha 2, collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1	
251	2262	AA859757	hh	collagen, type V, alpha 1, procollagen, type V, alpha 1	EST, Weakly similar to CGH1V collagen alpha 1(V) chain precursor [H.sapiens], Homo sapiens cDNA FLJ30442 fis, clone BRACE2009212, Homo sapiens proline-rich acidic protein mRNA, complete cds, Mus musculus, clone IMAGE:3490511, mRNA, partial cds, collagen, type V, alpha 1, collagen, type XI, alpha 1, endoplasmic reticulum chaperone SIL1, homolog of yeast, hypothetical protein MGC2705, procollagen, type V, alpha 1, procollagen, type V, alpha 3, procollagen, type XI, alpha 1	



TABLE 3

SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2544	25237	NM_134452	r	collagen, type V, alpha 1, procollagen, type V, alpha 1	EST, Weakly similar to CGHU1V collagen alpha 1(V) chain precursor [H.sapiens], Homo sapiens cDNA FLJ30442 fis, clone BRACE2009212, Homo sapiens proline-rich acidic protein mRNA, complete cds, Mus musculus, clone IMAGE:3490511, mRNA, partial cds, collagen, type V, alpha 1, collagen, type XI, alpha 1, endoplasmic reticulum chaperone SIL1, homolog of yeast, hypothetical protein MGC2705, procollagen, type V, alpha 1, procollagen, type V, alpha 3, procollagen, type XI, alpha 1
1399	15438	A1179399	e, g	collagen, type V, alpha 2, procollagen, type V, alpha 2	EST, Weakly similar to CGHU2V collagen alpha 2(V) chain precursor [H.sapiens], EST, Weakly similar to I49607 procollagen type V alpha 2 - mouse [M.musculus], ESTs, Weakly similar to I49607 procollagen type V alpha 2 - mouse [M.musculus], ESTs, Weakly similar to S41067 collagen alpha 1(III) chain - rat [R.norvegicus], Mus musculus, Similar to putative protein phosphatase 1 nuclear targeting subunit, clone IMAGE:3157989, mRNA, partial cds, RIKEN cDNA 2810002D19 gene, collagen, type V, alpha 2, procollagen, type III, alpha 1, procollagen, type V, alpha 2
2050	21443	NM_019262	kk, ll	complement component 1, q subcomponent, beta polypeptide	
2050	21444	NM_019262	jj, kk	complement component 1, q subcomponent, beta polypeptide	
2304	1727	NM_031642	jj, kk	core promoter element binding protein	DNA segment, Chr 12, ERATO Doi 427, expressed, EST, Moderately similar to core promoter element binding protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to core promoter element binding protein [Rattus norvegicus] [R.norvegicus], Kruppel-like factor 7 (ubiquitous), core promoter element binding protein
2040	15347	NM_019222	ll	coronin, actin binding protein 1B, coronin, actin-binding protein, 1B	ESTs, Moderately similar to CO1B_RAT Coronin 1B (Coronin 2) [R.norvegicus], coronin 6, coronin, actin binding protein 1B, coronin, actin binding protein 1C, coronin, actin binding protein, 1C, hypothetical protein DKFZp762166
1739	4467	NM_012529	f, g	creatine kinase, brain	
1739	4468	NM_012529	g	creatine kinase, brain	
1742	20357	NM_012534	cc, dd	crystallin, alpha A	crystallin, alpha A, expressed sequence A1323437

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1829	13723	NM_012935	aa, bb	crystallin, alpha B	ESTs, Moderately similar to T46637 transcription factor 1, neural - rat [R.norvegicus], ESTs, Weakly similar to A35804 nucleolin [H.sapiens], ESTs, Weakly similar to alpha-crystallin chain B [M.musculus], Homo sapiens mRNA; cDNA DKFZp434E0922 (from clone DKFZp434E0922), Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:281000318:myelin transcription factor 1-like, full insert sequence, crystallin, alpha B, myelin transcription factor 1-like, nucleolin	
1830	487	NM_012937	n	crystallin, beta B2	EST, Highly similar to CRB2_MOUSE BETA CRYSTALLIN B2 (BP) [R.norvegicus],	
2312	8844	NM_031690	b	crystallin, beta B3	EST, Weakly similar to A Chain A, The N-Terminal Domain Of Beta-B2-Crystallin	
2035	18572	NM_019201	n, o	C-terminal binding protein 1	Resembles The Putative Ancestral Homodimer [M.musculus], Homo sapiens, clone IMAGE:3542716, mRNA, partial cds, crystallin, beta B2	
2035	18573	NM_019201	f, g	C-terminal binding protein 1	absent in melanoma 1, absent in melanoma 1-like, crystallin, beta B3	
1657	25041	D14014	f	cyclin D1, cyclin D1 (PRAD1; parathyroid adenomatosis 1)	C-terminal binding protein 1, Homo sapiens mRNA; cDNA DKFZp434B0914 (from clone DKFZp434B0914); partial cds	
2677	24232	X75207	aa, bb	cyclin D1, cyclin D1 (PRAD1; parathyroid adenomatosis 1)	C-terminal binding protein 1, Homo sapiens mRNA; cDNA DKFZp434B0914 (from clone DKFZp434B0914); partial cds	
1825	20757	NM_012923	cc, dd	cyclin G, cyclin G1	EST, Moderately similar to JC2342 cyclin D1 - rat [R.norvegicus], cyclin D1, cyclin D1 (PRAD1; parathyroid adenomatosis 1)	
1468	14430	A1230798	r	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	EST, Moderately similar to JC2342 cyclin D1 - rat [R.norvegicus], cyclin D1, cyclin D1 (PRAD1; parathyroid adenomatosis 1)	
1804	2853	NM_012838	n, o	cystatin B, cystatin B (stefin B)	ESTs, Weakly similar to CGG1_RAT Cyclin G1 (Cyclin G) [R.norvegicus], cyclin G, cyclin G2, cyclin I	
1482	24327	A1231292	gg	cystatin C, cystatin C (amyloid angiopathy and cerebral hemorrhage)	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	
2483	1892	NM_057144	ff, kk	cysteine and glycine-rich protein 3 (cardiac LIM protein), cysteine-rich protein 3	cystatin B, cystatin B (stefin B)	
					ESTs, Moderately similar to CYTC_MOUSE CYSTATIN C PRECURSOR [M.musculus], ESTs, Weakly similar to CYTC_MOUSE CYSTATIN C PRECURSOR [M.musculus], RIKEN cDNA 1110017E11 gene, RIKEN cDNA 9230101F08 gene, cystatin C, cystatin C (amyloid angiopathy and cerebral hemorrhage), cystatin D, cystatin S, cystatin SA, cystatin SN	
					RIKEN cDNA 120007O21 gene, cysteine and glycine-rich protein 3 (cardiac LIM protein), cysteine-rich protein 3	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
					EST, Weakly similar to COX4_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR [H.sapiens], ESTs, Moderately similar to COX4_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR [H.sapiens], cytochrome c oxidase subunit IV isoform 1, cytochrome c oxidase, subunit IVa	
1968	14694	NM_017202	aa	cytochrome c oxidase subunit IV isoform 1, cytochrome c oxidase, subunit IVa		
2383	21866	NM_053472	u, v	cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase, subunit IVb	cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase, subunit IVb	
1138	23574	A104520	hh	cytochrome c oxidase subunit VIa polypeptide 1, cytochrome c oxidase, subunit VI a, polypeptide 1		
1743	20704	NM_012541	aa, bb	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	
1831	190	NM_012940	j, k	cytochrome P450, 1b1, benz[a]anthracene inducible, cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	cytochrome P450, 1b1, benz[a]anthracene inducible, cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	
2281	4010	NM_031543	u, v	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)		
2281	4011	NM_031543	v	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)		
1832	20928	NM_012941	l, m	cytochrome P450, 51, cytochrome P450, 51 (lanosterol 14-alpha-demethylase)	cytochrome P450, 51, cytochrome P450, 51 (lanosterol 14-alpha-demethylase)	
1708	20714	M14972	s, t	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	EST, Moderately similar to i65981 fatty acid omega-hydroxylase [H.sapiens], Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837, mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11, expressed sequence A1314743	
1909	20921	NM_016999	s, t	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	EST, Moderately similar to i65981 fatty acid omega-hydroxylase [H.sapiens], Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837, mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11, expressed sequence A1314743	

TABLE 3

SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1744	1762 NM_012543	f		D site albumin promoter binding protein, D site of albumin promoter (albumin D-box) binding protein	D site albumin promoter binding protein, D site of albumin promoter (albumin D-box) binding protein, RIKEN cDNA 2310028D20 gene
1744	1763 NM_012543	hh		D site albumin promoter binding protein, D site of albumin promoter (albumin D-box) binding protein	D site albumin promoter binding protein, D site of albumin promoter (albumin D-box) binding protein, RIKEN cDNA 2310028D20 gene
2174	17226 NM_024131	b, c, u, v		D-dopachrome tautomerase	D-dopachrome tautomerase, EST, Moderately similar to DOPD_HUMAN D-DOPACHROME TAUTOMERASE [H.sapiens]
2174	17227 NM_024131	c		D-dopachrome tautomerase	D-dopachrome tautomerase, EST, Moderately similar to DOPD_HUMAN D-DOPACHROME TAUTOMERASE [H.sapiens]
2691	18352 Z12298	aa, bb		decorin	RIKEN cDNA 553060M07 gene, decorin, expressed sequence C85409, extracellular matrix protein 2, female organ and adipocyte specific
					EST, Weakly similar to diacylglycerol kinase zeta [Rattus norvegicus]
					[R.norvegicus], ESTs, Highly similar to KDGA MOUSE DIACYLGLYCEROL KINASE, ALPHA [M.musculus], ESTs, Weakly similar to diacylglycerol kinase [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to KDGA MOUSE DIACYLGLYCEROL KINASE, ALPHA [M.musculus], diacylglycerol kinase, alpha (80 kDa), diacylglycerol kinase, gamma 3, diacylglycerol kinase, iota, diacylglycerol kinase, zeta (104kD)
2260	1638 NM_031143	d, e, ii, kk		diacylglycerol kinase zeta, diacylglycerol kinase, zeta (104kD)	ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrolase 1, dimethylarginine dimethylaminohydrolase 2
1	19424 AA850922	h, l		dimethylarginine dimethylaminohydrolase 1	ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrolase 1, dimethylarginine dimethylaminohydrolase 2
3	19421 AA945152	bb		dimethylarginine dimethylaminohydrolase 1	ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrolase 1, dimethylarginine dimethylaminohydrolase 2
					ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrolase 1, dimethylarginine dimethylaminohydrolase 2
2104	19423 NM_022297	u, v		dimethylarginine dimethylaminohydrolase 1	dimethylarginine dimethylaminohydrolase 1, dimethylarginine dimethylaminohydrolase 2

TABLE 3

SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
774	7785 AI008758		jj, kk	dipeptidylpeptidase 4, dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)	ESTs, Weakly similar to DPP4 MOUSE DIPEPTIDYL PEPTIDASE IV [M.musculus], ESTs, Weakly similar to DPP4_RAT Dipeptidyl peptidase IV (DPP IV) (GP110 glycoprotein) (Bile canaliculus domain-specific membrane glycoprotein) [R.norvegicus], dipeptidylpeptidase 4, dipeptidylpeptidase 8, fibroblast activation protein, fibroblast activation protein, alpha
153	6054 AA818658		p, q, ee, ff	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), heparin binding epidermal growth factor-like growth factor	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), heparin binding epidermal growth factor-like growth factor
1833	223 NM_012945		a, p, q, ee, ff	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), heparin binding epidermal growth factor-like growth factor	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), heparin binding epidermal growth factor-like growth factor
1796	1952 NM_012788		gg	discs, large (Drosophila) homolog 1, discs, large homolog 1 (Drosophila)	Mus musculus mRNA for mDLG6B, complete cds, discs, large (Drosophila) homolog 1, discs, large (Drosophila) homolog 5, discs, large homolog 1 (Drosophila), discs, large homolog 5 (Drosophila), guanylate kinase 1
1951	24106 NM_017141		s, t, bb	DNA polymerase beta, polymerase (DNA directed), beta	Mus musculus, Similar to DNA polymerase beta, clone MGC:6386 IMAGE:3581916, mRNA, complete cds, polymerase (DNA directed), beta
1951	24107 NM_017141		ll	DNA polymerase beta, polymerase (DNA directed), beta	Mus musculus, Similar to DNA polymerase beta, clone MGC:6386 IMAGE:3581916, mRNA, complete cds, polymerase (DNA directed), beta
1652	18686 D00729		g, hh	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
1999	18687 NM_017306		hh	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
1950	492 NM_017140		i, m, n, aa	dopamine receptor 3, dopamine receptor D3	dopamine receptor 3, dopamine receptor D3
2218	1719 NM_031024		jj, kk	drebrin 1	drebrin 1
2427	15996 NM_053769		cc, dd	dual specificity phosphatase 1, protein tyrosine phosphatase, non-receptor type 16	Mus musculus, clone MGC:11703 IMAGE:3964527, mRNA, complete cds, RIKEN cDNA 2310076D10 gene, RIKEN cDNA 4930527G07 gene, dual specificity phosphatase 1, expressed sequence BB104621, protein tyrosine phosphatase, non-receptor type 16

TABLE 3

SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1797	24113	NM_012791	e	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	ESTs, Moderately similar to DYRA_RAT Dual-specificity tyrosine-phosphorylation regulated kinase 1A (Protein Kinase minibrain homolog) (MNBH) (RP86) (Dual specificity YAK1-related kinase) [R.norvegicus], ESTs, Weakly similar to DYRK MOUSE DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLATION REGULATED KINASE [M.musculus], Mus musculus, clone MGC:6699 IMAGE:3584001, mRNA, complete cds, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a
1797	18135	NM_012791	e, gg, ll	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	ESTs, Moderately similar to DYRA_RAT Dual-specificity tyrosine-phosphorylation regulated kinase 1A (Protein Kinase minibrain homolog) (MNBH) (RP86) (Dual specificity YAK1-related kinase) [R.norvegicus], ESTs, Weakly similar to DYRK MOUSE DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLATION REGULATED KINASE [M.musculus], Mus musculus, clone MGC:6699 IMAGE:3584001, mRNA, complete cds, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a
2415	1118	NM_053655	u	dynamain 1-like	ESTs, Moderately similar to dynamain 2 [Mus musculus] [M.musculus], Mus musculus, Similar to KIAA0820 protein, clone MGC:37713 IMAGE:5066120, mRNA, complete cds, Mus musculus, Similar to dynamain 1-like, clone MGC:41233 IMAGE:1395338, mRNA, complete cds, dynamain 1-like, dynamain 2
1895	1693	NM_013199	gg	dynamain 2	ESTs, Highly similar to A53165 dynamain II isoform aa - rat [R.norvegicus], ESTs, Moderately similar to dynamain 2 [Mus musculus] [M.musculus], Mus musculus, Similar to KIAA0820 protein, clone MGC:37713 IMAGE:5066120, mRNA, complete cds, Mus musculus, Similar to dynamain 1-like, clone MGC:41233 IMAGE:1395338, mRNA, complete cds, RIKEN cDNA 1200011N24 gene, dynamain 2
1775	425	NM_012698	hh	dystrophin (muscular dystrophy, Duchenne and Becker types), dystrophin, muscular dystrophy	dystrobrevin alpha, dystrobrevin, beta, utrophin
1746	23868	NM_012551	a, h, l, p, q, y, z, ee, ff	early growth response 1	early growth response 1, expressed sequence A1835008
1746	23869	NM_012551	a, h, l, p, q, y, z	early growth response 1	early growth response 1, expressed sequence A1835008
1746	23871	NM_012551	p, q, y, z, ii	early growth response 1	early growth response 1, expressed sequence A1835008

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1746	23872	NM_012551	p, q, y, z	early growth response 1	early growth response 1, expressed sequence A1835008	
2020	16227	NM_019137	i, m	early growth response 4	RIKEN cDNA 493053M09 gene, early growth response 4 ESTs, Weakly similar to CD39 MOUSE VASCULAR ATP-DIPHOSPHOHYDROLASE [M.musculus], RIKEN cDNA 2010320H07 gene, ectonucleoside triphosphate diphosphohydrolase 1, ectonucleoside triphosphate diphosphohydrolase 3, lysosomal apyrase-like 1	
1450	23042	AI230130	s, t, ii	ectonucleoside triphosphate diphosphohydrolase 2		
2476	9528	NM_057104	r	ectonucleotide pyrophosphatase/phosphodiesterase 2, ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	ectonucleotide pyrophosphatase/phosphodiesterase 2, ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) EGL nine homolog 3 (C. elegans), ESTs, Moderately similar to A53770 growth factor-responsive protein, vascular smooth muscle - rat [R.norvegicus], ESTs, Weakly similar to A53770 growth factor-responsive protein, vascular smooth muscle - rat [R.norvegicus], Mus musculus, Similar to EGL nine homolog 3 (C. elegans), clone MGC:36685 IMAGE:5371854, mRNA, complete cds, egl nine homolog 1 (C. elegans), egl nine homolog 3 (C. elegans)	
2067	1323	NM_019371	c, aa, bb, ii	EGL nine homolog 3 (C. elegans), egl nine homolog 3 (C. elegans)	EGL nine homolog 3 (C. elegans), ESTs, Moderately similar to A53770 growth factor-responsive protein, vascular smooth muscle - rat [R.norvegicus], ESTs, Weakly similar to A53770 growth factor-responsive protein, vascular smooth muscle - rat [R.norvegicus], Mus musculus, Similar to EGL nine homolog 3 (C. elegans), clone MGC:36685 IMAGE:5371854, mRNA, complete cds, egl nine homolog 1 (C. elegans), egl nine homolog 3 (C. elegans)	
2067	1324	NM_019371	f, g, aa, bb, kk	EGL nine homolog 3 (C. elegans), egl nine homolog 3 (C. elegans)	EST, Moderately similar to Peroxisomal enoyl hydratase-like protein; enoyl hydratase-like protein, peroxisomal [Rattus norvegicus] [R.norvegicus], enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, peroxisomal	
2143	20925	NM_022594	g, hh	enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, peroxisomal	EST, Highly similar to putative protein-tyrosine kinase [Homo sapiens] [H.sapiens], Eph receptor B1, Eph receptor B2, Eph receptor B3, EphB1, expressed sequence AW456895, expressed sequence AW488255	
2644	2464	X13411	u, v	Eph receptor B2, EphB2	epithelial membrane protein 1	
1805	338	NM_012843	r	epithelial membrane protein 1	epoxide hydrolase 1, microsomal, epoxide hydrolase 1, microsomal (xenobiotic)	
1806	17541	NM_012844	c, d	epoxide hydrolase 1, microsomal (xenobiotic)		

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SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2362	24420	NM_033539	jj, kk, ll	eukaryotic translation elongation factor 1 alpha 2	EST, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain - rat [R.norvegicus], ESTs, Highly similar to EFHU1 translation elongation factor eEF-1 alpha-1 chain [H.sapiens], ESTs, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain - rat [R.norvegicus], G1 to S phase transition 1, G1 to phase transition 1, G1 to phase transition 2, eukaryotic translation elongation factor 1 alpha 1	
1980	17561	NM_017245	l, m	eukaryotic translation elongation factor 2	ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs, Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], ESTs, Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], G elongation factor, Mus musculus, Similar to elongation factor G2, clone MGC:28160 IMAGE:3984129, mRNA, complete cds, U5 small nuclear ribonucleoprotein 116 kDa, U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 2, expressed sequence A1451340	
1980	17563	NM_017245	h, l	eukaryotic translation elongation factor 2	ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs, Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], ESTs, Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], G elongation factor, Mus musculus, Similar to elongation factor G2, clone MGC:28160 IMAGE:3984129, mRNA, complete cds, U5 small nuclear ribonucleoprotein 116 kDa, U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 2, expressed sequence A1451340	
1206	23152	A1169170	r	eukaryotic translation initiation factor 4A, isoform 2	ESTs, Weakly similar to EUKARYOTIC INITIATION FACTOR 4A-II [M.musculus], eukaryotic translation initiation factor 4A, isoform 2	
2075	18713	NM_020075	p, q, s, t	eukaryotic translation initiation factor 5	DNA segment, Chr 1, ERATO Doi 692, expressed, ESTs, Highly similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 5 [R.norvegicus], KIAA1856 protein, eukaryotic translation initiation factor 5	
2075	18715	NM_020075	ee, ff	eukaryotic translation initiation factor 5	DNA segment, Chr 1, ERATO Doi 692, expressed, ESTs, Highly similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 5 [R.norvegicus], KIAA1856 protein, eukaryotic translation initiation factor 5	
2184	16476	NM_024162	aa	fatty acid binding protein 3, muscle and heart (mammary-derived binding protein 3, muscle and heart (mammary-derived growth inhibitor)	EST, Moderately similar to FABH MOUSE FATTY ACID-BINDING PROTEIN, HEART [M.musculus], fatty acid binding protein 3, muscle and heart, fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	



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431	20985	AA893242	II	fatty acid Coenzyme A ligase, long chain 2, fatty-acid-Coenzyme A ligase, long-chain 2	ES1s, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipidosis-related protein lipidosin	
431	20986	AA893242	II	fatty acid Coenzyme A ligase, long chain 2, fatty-acid-Coenzyme A ligase, long-chain 2	ES1s, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipidosis-related protein lipidosin	
972	20983	AI044900	a, h, l, ee, ff, kk	fatty acid Coenzyme A ligase, long chain 2, fatty-acid-Coenzyme A ligase, long-chain 2	ES1s, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipidosis-related protein lipidosin	

TABLE 3						Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1668	20984	D90109	II	fatty acid Coenzyme A ligase, long chain 2, fatty-acid-Coenzyme A ligase, long-chain 2	ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipidosis-related protein lipidosis	
2410	13005	NM_053623	j, k, y, z	fatty acid-Coenzyme A ligase, long chain 4, fatty-acid-Coenzyme A ligase, long-chain 4		
1319	10182	A1176185	p, q, gg	FBJ osteosarcoma oncogene, v-fos FBJ murine osteosarcoma viral oncogene homolog	FBJ murine osteosarcoma viral oncogene homolog B, FBJ osteosarcoma oncogene, FBJ osteosarcoma oncogene B, v-fos FBJ murine osteosarcoma viral oncogene homolog	
2641	10181	X06769	p, q	FBJ osteosarcoma oncogene, v-fos FBJ murine osteosarcoma viral oncogene homolog	FBJ murine osteosarcoma viral oncogene homolog B, FBJ osteosarcoma oncogene, FBJ osteosarcoma oncogene B, v-fos FBJ murine osteosarcoma viral oncogene homolog	
2440	20868	NM_053843	kk	Fc fragment of IgG, low affinity IIIa, receptor for (CD16), Fc receptor, IgG, low affinity III		
2440	20869	NM_053843	w, x, kk	Fc fragment of IgG, low affinity IIIa, receptor for (CD16), Fc receptor, IgG, low affinity III		
2359	12364	NM_033351	e, y, z, ee, ff	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter	
2359	12365	NM_033351	e	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter	
1944	21662	NM_017126	a, ee, ff	ferredoxin 1	ferredoxin 1, similar to RIKEN cDNA B230118G17 gene	
1944	21663	NM_017126	a, h, l, p, q, y, z, ee, ff	ferredoxin 1	ferredoxin 1, similar to RIKEN cDNA B230118G17 gene	
2119	8211	NM_022500	jj, kk	ferritin light chain 1, ferritin, light polypeptide	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus], RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide	

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2119	8212	NM_022500	h, l, kk, ll	ferritin light chain 1, ferritin, light polypeptide	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus], RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide	
2600	8210	S61960	jj, kk	ferritin light chain 1, ferritin, light polypeptide	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus], RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide	
1747	6477	NM_012559	z	fibrinogen, gamma polypeptide		
1747	6478	NM_012559	y, z	fibrinogen, gamma polypeptide		
2091	20177	NM_021867	d, jj, kk	fibroblast growth factor 16	fibroblast growth factor 16	
1729	13489	M91599	cc, dd	fibroblast growth factor receptor 4		
2022	5618	NM_019143	s, t	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1	
2022	5622	NM_019143	n, o	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1	
2025	6451	NM_019153	f, g	fibulin 5		
1318	6782	A1176170	e	FK506 binding protein 1A (12kD), FK506 binding protein 1a (12 kDa)	FK506 binding protein 10 (65 kDa), FK506 binding protein 1A (12kD), FK506 binding protein 1a (12 kDa), FK506 binding protein 5, FK506 binding protein 7 (23 kDa), FK506 binding protein 8 (38 kDa)	
2155	24346	NM_022701	gg	flotillin 1	flotillin 1	
1696	25359	L13202	n, o	forkhead box D3		
2309	18403	NM_031677	d, jj, kk	four and a half LIM domains 2	EST, Weakly similar to four and a half LIM domains 2 [Rattus norvegicus] [R.norvegicus], activator of CREM in testis, four and a half LIM domains 2, four and a half LIM domains 3, vascular Rab-GAP/TBC-containing	
2411	1228	NM_053625	j, k	G elongation factor, mitochondrial elongation factor G		
2358	23715	NM_033237	j, k, y, z, jj, kk	galanin		
2496	506	NM_080586	ii	gamma-aminobutyric acid (GABA) A receptor, gamma 1, gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 1	gamma-aminobutyric acid (GABA) A receptor, gamma 2, gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 1	

TABLE 3

SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1749	482 NM_012567	s, t		gap junction membrane channel protein alpha 1, gap junction protein, alpha 1, 43kD (connexin 43)	gap junction membrane channel protein alpha 1, gap junction protein, alpha 1, 43kD (connexin 43)
2051	1143 NM_019280	w, x		gap junction membrane channel protein alpha 5, gap junction protein, alpha 5, 40kD (connexin 40)	gap junction membrane channel protein alpha 5, gap junction protein, alpha 5, 40kD (connexin 40)
2031	23481 NM_019185	aa, bb		GATA binding protein 6	GATA binding protein 5, GATA binding protein 6
1934	1383 NM_017088	II		GDP dissociation inhibitor 1, guanosine diphosphate (GDP) dissociation inhibitor 1	GDP dissociation inhibitor 1, guanosine diphosphate (GDP) dissociation inhibitor 2
2374	18949 NM_053345	ii		general transcription factor II A, 2 (12kD subunit), general transcription factor IIA, 2 (12kD subunit)	general transcription factor II A, 2 (12kD subunit), general transcription factor IIA, 2 (12kD subunit)
1748	619 NM_012565	I, m, n, o		glucokinase, glucokinase (hexokinase 4, maturity onset diabetes of the young 2)	
2293	5496 NM_031589	a, ee, ff		glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1	Mus musculus, Similar to solute carrier family 37 (glycerol-3-phosphate transporter), member 1, clone MGC:28167 IMAGE:3985469, mRNA, complete cds, glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1, solute carrier family 37 (glycerol-3-phosphate transporter), member 1
2293	5497 NM_031589	ii		glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1	Mus musculus, Similar to solute carrier family 37 (glycerol-3-phosphate transporter), member 1, clone MGC:28167 IMAGE:3985469, mRNA, complete cds, glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1, solute carrier family 37 (glycerol-3-phosphate transporter), member 1
2597	15693 S56679	aa, bb		glutamate receptor, ionotropic, AMPA 1, glutamate receptor, ionotropic, AMPA1 (alpha 1)	glutamate receptor, ionotropic, AMPA 1, glutamate receptor, ionotropic, AMPA1 (alpha 1)
1911	24676 NM_017010	aa, bb		glutamate receptor, ionotropic, N-methyl D-aspartate 1, glutamate receptor, ionotropic, NMDA1 (zeta 1)	
1929	11152 NM_017073	c, s, t, kk		glutamate-ammonia ligase (glutamine synthase), glutamine synthetase	
1929	11153 NM_017073	y, kk		glutamate-ammonia ligase (glutamine synthase), glutamine synthetase	
1998	14004 NM_017305	aa, bb		glutamate-cysteine ligase, modifier subunit, glutamate-cysteine ligase, modifier subunit	glutamate-cysteine ligase, modifier subunit, glutamate-cysteine ligase, modifier subunit

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544	5206	AA925755	II	glutaminase	ESTs, Highly similar to GLSK RAT GLUTAMINASE, KIDNEY ISOFORM PRECURSOR [R.norvegicus], ESTs, Moderately similar to GLSK_HUMAN GLUTAMINASE, KIDNEY ISOFORM, MITOCHONDRIAL PRECURSOR (GLS) (L-GLUTAMINE AMIDOHYDROLASE) (K-GLUTAMINASE) [H.sapiens], Homo sapiens glutaminase isoform M precursor, mRNA, complete cds, expressed sequence A1314027, glutaminase expressed sequence A1266902, expressed sequence D17825, glutaryl-Coenzyme A dehydrogenase
1150	23596	A1105435	bb	glutaryl-Coenzyme A dehydrogenase	ESTs, Weakly similar to GSHC_RAT Glutathione peroxidase (GSHPX-1) (Cellular glutathione peroxidase) [R.norvegicus], glutathione peroxidase 1, glutathione peroxidase 2, glutathione peroxidase 2 (gastrointestinal)
2202	1852	NM_030826	aa, gg	glutathione peroxidase 1	ESTs, Weakly similar to GSHH_RAT Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (PHGPx) (GPX-4) [R.norvegicus], RIKEN cDNA 2310016C16 gene, RIKEN cDNA 3110050F08 gene, glutathione peroxidase 4, glutathione peroxidase 4 (phospholipid hydroperoxidase)
1958	17686	NM_017165	hh	glutathione peroxidase 4, glutathione peroxidase 4 (phospholipid hydroperoxidase)	
1912	21013	NM_017014	b	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2	
1799	961	NM_012796	g	glutathione S-transferase theta 2, glutathione S-transferase, theta 2	glutathione S-transferase theta 2, glutathione S-transferase, theta 2
1910	8417	NM_017008	aa	glyceraldehyde-3-phosphate dehydrogenase	ESTs, Moderately similar to G3P MOUSE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE [M.musculus], Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3000002C10:glyceraldehyde-3-phosphate dehydrogenase, full insert sequence, RIKEN cDNA 4930448K20 gene, glyceraldehyde-3-phosphate dehydrogenase
1784	25650	NM_012736	d	glycerol phosphate dehydrogenase 1, mitochondrial, glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610001M21:glycerol phosphate dehydrogenase 1, mitochondrial, full insert sequence, glycerol phosphate dehydrogenase 1, mitochondrial, glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
2513	19456	NM_133298	h, l, w, x	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
2513	4048	NM_133298	x	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
2513	4049	NM_133298	c, h, l, n, o, w, x	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
143	16756	AA818089	II	glycyl-tRNA synthetase	glycyl-tRNA synthetase	
2203	21746	NM_030828	C	glypican 1	glypican 1	
2019	15975	NM_019132	ii	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus, GNAS complex locus	ESTs, Moderately similar to S34421 GTP-binding regulatory protein Gs alpha chain [H.sapiens], GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus, GNAS complex locus, RIKEN cDNA 5530400H20 gene, Sang, XLas protein	
12	21152	X14848	bb	golgi SNAP receptor complex member 1	Homo sapiens, Similar to golgi SNAP receptor complex member 1, clone MGC:13657 IMAGE:4250494, mRNA, complete cds, golgi SNAP receptor complex member 1	
1941	20745	NM_017113	f, g	granulin	granulin	
1941	20746	NM_017113	j, cc, dd, gg	granulin	granulin	
2173	352	NM_024127	p, q	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	
2173	353	NM_024127	q, ee, ff, gg	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	
2173	354	NM_024127	p, q, ee, ff	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	
1026	17506	A1070068	p, q	growth arrest and DNA-damage-inducible, beta	growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible, beta	
2473	25290	NM_057100	d, u, v	growth arrest specific 6, growth arrest-specific 6	ESTs, Highly similar to growth arrest specific 6 [Rattus norvegicus] [R.norvegicus], growth arrest specific 6, growth arrest-specific 6	
2301	15767	NM_031623	aa, bb, jj, kk, ll	growth factor receptor bound protein 14, growth factor receptor-bound protein 14	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein, growth factor receptor bound protein 10, growth factor receptor bound protein 14, growth factor receptor-bound protein 10, growth factor receptor-bound protein 14	
1902	1396	NM_013222	d	growth factor, augment of liver regeneration (ERV1 homolog, S. cerevisiae), growth factor, erv1 (S. cerevisiae)-like (augment of liver regeneration)	growth factor, augment of liver regeneration (ERV1 homolog, S. cerevisiae), growth factor, erv1 (S. cerevisiae)-like (augment of liver regeneration)	
815	17524	A1010568	jj, kk	growth hormone receptor	growth hormone receptor	
1936	10886	NM_017094	ii	growth hormone receptor	growth hormone receptor	
1936	10887	NM_017094	jj, kk	growth hormone receptor	growth hormone receptor	
1936	10888	NM_017094	e, r, hh	growth hormone receptor	growth hormone receptor	
2290	942	NM_031577	u	growth hormone releasing hormone	growth hormone releasing hormone	

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1807	1249	NM_012850	u, v	growth hormone releasing hormone receptor	growth hormone releasing hormone receptor
2199	862	NM_024487	hh	GrpE-like 1, mitochondrial GrpE-like protein co-chaperone	
2187	15349	NM_024356	a, y, z	GTP cyclohydrolase 1, GTP cyclohydrolase 1 (dopa-responsive dystonia)	GTP cyclohydrolase 1, GTP cyclohydrolase 1 (dopa-responsive dystonia)
2187	15353	NM_024356	j, k, y, z, ii	GTP cyclohydrolase 1, GTP cyclohydrolase 1 (dopa-responsive dystonia)	GTP cyclohydrolase 1, GTP cyclohydrolase 1 (dopa-responsive dystonia)
1296	19118	A1175281	hh	guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase	expressed sequence AA571402, guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase
1798	16947	NM_012793	b, u, v, jj, kk	guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase	ESTs, Moderately similar to guanine nucleotide binding protein (G protein) alpha 12 [Rattus norvegicus] [R.norvegicus], guanine nucleotide binding protein (G protein), alpha 13, guanine nucleotide binding protein, alpha 12, guanine nucleotide binding protein, alpha 13
2220	690	NM_031034	w, x	guanine nucleotide binding protein (G protein) alpha 12, guanine nucleotide binding protein, alpha 12	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3, guanine nucleotide binding protein, alpha inhibiting 3
1870	19949	NM_013106	l, m	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3, guanine nucleotide binding protein, alpha inhibiting 3	ESTs, Weakly similar to C Chain C, Apaf-1 Card In Complex With Prodomain Of Procaspase-9 {SUB 1-95 [H.sapiens], Homo sapiens mRNA expressed only in placental villi, clone SMAP5, PWP2 periodic tryptophan protein homolog (yeast), Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds, guanine nucleotide binding protein (G protein), beta polypeptide 2, guanine nucleotide binding protein, beta 2
139	2143	AA817892	r	guanine nucleotide binding protein (G protein), beta polypeptide 2, guanine nucleotide binding protein, beta 2	EST, Weakly similar to B33928 GTP-binding protein beta chain homolog [H.sapiens], EST, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 [H.sapiens], Homo sapiens cDNA: FLJ21913 fis, clone HEP03888, Mus musculus, Similar to hypothetical protein FLJ10385, clone MGC:28622 IMAGE:4220923, mRNA, complete cds, expressed sequence AL033335, guanine nucleotide binding protein (G protein), beta polypeptide 1-like, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1
2506	14959	NM_130734	w, x	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1	

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1250	14960	A1171319	w, x	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1	EST, weakly similar to B33928 GTP-binding protein beta chain homolog [H.sapiens], EST, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 [H.sapiens], Homo sapiens cDNA: FLJ21913 fis, clone HEP03888, Mus musculus, Similar to hypothetical protein FLJ10385, clone MGC:28622 IMAGE:4220923, mRNA, complete cds, SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1, expressed sequence AL033335, guanine nucleotide binding protein (G protein), beta polypeptide 1-like, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1	
2175	1879	NM_024138	l, m	guanine nucleotide binding protein (G protein), gamma 7, guanine nucleotide binding protein (G protein), gamma 7 subunit	guanine nucleotide binding protein (G protein), gamma 12, guanine nucleotide binding protein (G protein), gamma 7	
1750	16025	NM_012578	p, q	H1 histone family, member 0	H1 histone family, member 0, H1 histone family, member O (oocyte-specific)	
1750	16026	NM_012578	p, q, s, t, ee, ff	H1 histone family, member 0	H1 histone family, member 0, H1 histone family, member O (oocyte-specific)	
1964	1488	NM_017182	h	H2A histone family, member Y	H2A histone family, member Y, RIKEN cDNA 4933432H23 gene	
2147	17661	NM_022674	d, gg	H2A histone family, member Z	EST, Weakly similar to histone H2A.F/Z variant [Homo sapiens] [H.sapiens], ESTs, Highly similar to S03644 histone H2A.Z - rat [R.norvegicus], ESTs, Weakly similar to H2AZ_HUMAN HISTONE H2A [H.sapiens], H2A histone family, member Z, Homo sapiens cDNA FLJ32241 fis, clone PLACE605231, RIKEN cDNA C530002L11 gene, histone H2A.F/Z variant	
1834	5033	NM_012966	s, t	heat shock 10 kDa protein 1 (chaperonin 10), heat shock 10kD protein 1 (chaperonin 10)	ESTs, Weakly similar to S47532 chaperonin groES [H.sapiens], expressed sequence AW108200, heat shock 10 kDa protein 1 (chaperonin 10), heat shock 10kD protein 1 (chaperonin 10)	
1834	5034	NM_012966	ee, ff	heat shock 10 kDa protein 1 (chaperonin 10), heat shock 10kD protein 1 (chaperonin 10)	ESTs, Weakly similar to S47532 chaperonin groES [H.sapiens], expressed sequence AW108200, heat shock 10 kDa protein 1 (chaperonin 10), heat shock 10kD protein 1 (chaperonin 10)	
2505	11709	NM_130431	s	heat shock 27kD protein 2	EST, Moderately similar to heat shock 27kD protein 2 [Rattus norvegicus] [R.norvegicus], heat shock 27kD protein 2	



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1707	1466	M14050	e	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	EST, Weakly similar to GR78_RAT 78 KD GLUCOSE-REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN) (BIP) (STEROIDOGENESIS-ACTIVATOR POLYPEPTIDE) [R.norvegicus], expressed sequence AL022860, heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	
2185	17764	NM_024351	e, p, r, ee, ff	heat shock 70kD protein 8	EST, Moderately similar to HS7C_HUMAN HEAT SHOCK COGNATE 71 KDA PROTEIN [H.sapiens], EST, Weakly similar to A27077 dnaK-type molecular chaperone [H.sapiens], EST, Weakly similar to A45935 dnaK-type molecular chaperone hsc70 - mouse [M.musculus], ESTs, Moderately similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], ESTs, Weakly similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], heat shock 70kD protein 8	
2185	17765	NM_024351	e, p, q, r, ee, ff	heat shock 70kD protein 8	EST, Moderately similar to HS7C_HUMAN HEAT SHOCK COGNATE 71 KDA PROTEIN [H.sapiens], EST, Weakly similar to A27077 dnaK-type molecular chaperone [H.sapiens], EST, Weakly similar to A45935 dnaK-type molecular chaperone hsc70 - mouse [M.musculus], ESTs, Moderately similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], ESTs, Weakly similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], heat shock 70kD protein 8	
1402	16081	A1179610	a, p, q, r, y, z, gg, kk	heme oxygenase (decycling) 1	heme oxygenase (decycling) 1	
1751	16080	NM_012580	p, q, y, z, kk	heme oxygenase (decycling) 1	heme oxygenase (decycling) 1	
1389	18907	A1178971	c, v	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1	

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1406	1686	AI179971	c	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1	
1406	1687	AI179971	b, c, v	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1	
1869	1684	NM_013096	b, c, v	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1	
1869	1685	NM_013096	b, c, v	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID No.	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1869	1688	NM_013096	c	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1	
1869	1689	NM_013096	b, c, v	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1	
305	18897	AA875207	t	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence A1036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta	
839	17830	A1011943	c	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence A1036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta	
2356	25468	NM_033234	b, c, v	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence A1036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta	
2356	17829	NM_033234	c	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence A1036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta	
2356	17832	NM_033234	b, c, v	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence A1036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
875	6758	AI013394	d, jj, kk	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	EST, Highly similar to HSS2 MOUSE HEPARIN SULFATE N-DEACETYLASE/N-SULFOTRANSFERASE [M.musculus], ESTs, Weakly similar to HSS2 MOUSE HEPARIN SULFATE N-DEACETYLASE/N-SULFOTRANSFERASE [M.musculus], ESTs, Weakly similar to HSS2_HUMAN HEPARIN SULFATE N-DEACETYLASE/N-SULFOTRANSFERASE [H.sapiens], N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3, N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4, N-deacetylase/N-sulfotransferase 4, RIKEN cDNA 4930439H17 gene, heparan sulfate (glucosamine) 3-O-sulfotransferase 3A, heparan sulfate (glucosamine) 3-O-sulfotransferase 4	
1587	18151	AI237212	f, g, hh	hepatitis B virus x interacting protein	hepatitis B virus x interacting protein	
2269	4235	NM_031330	b, d, f, g, l, m	heterogeneous nuclear ribonucleoprotein A/B	DAZ associated protein 1, Musashi homolog 1 (Drosophila), Musashi homolog 2 (Drosophila), RIKEN cDNA 4933434H11 gene, expressed sequence AA959857, heterogeneous nuclear ribonucleoprotein A/B, musashi homolog 1 (Drosophila) ESTs, Highly similar to l52962 FBRNP [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP) [R.norvegicus], Homo sapiens cDNA: FLJ22720 fis, clone HSI14320, Mus musculus, Similar to TAR DNA binding protein, clone MGC:19284 IMAGE:4016437, mRNA, complete cds, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1	
1981	17501	NM_017248	l, m	heterogeneous nuclear ribonucleoprotein A1	ESTs, Highly similar to l52962 FBRNP [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP) [R.norvegicus], Homo sapiens cDNA: FLJ22720 fis, clone HSI14320, Mus musculus, Similar to TAR DNA binding protein, clone MGC:19284 IMAGE:4016437, mRNA, complete cds, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1	
1981	17502	NM_017248	l, m	heterogeneous nuclear ribonucleoprotein A1	ESTs, Highly similar to l52962 FBRNP [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP) [R.norvegicus], Homo sapiens cDNA: FLJ22720 fis, clone HSI14320, Mus musculus, Similar to TAR DNA binding protein, clone MGC:19284 IMAGE:4016437, mRNA, complete cds, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2482	2413	NM_057141	b, g, n, o, u, v	heterogeneous nuclear ribonucleoprotein K	ESTs, Highly similar to heterogeneous nuclear ribonucleoprotein K, isoform b; dC-stretch binding protein; transformation upregulated nuclear protein [Homo sapiens] [H.sapiens], ESTs, Weakly similar to heterogeneous nuclear ribonucleoprotein K [Rattus norvegicus] [R.norvegicus], heterogeneous nuclear ribonucleoprotein K, poly(rC) binding protein 3, poly(rC) binding protein 4	
2482	2416	NM_057141	t	heterogeneous nuclear ribonucleoprotein K	ESTs, Highly similar to heterogeneous nuclear ribonucleoprotein K, isoform b; dC-stretch binding protein; transformation upregulated nuclear protein [Homo sapiens] [H.sapiens], ESTs, Weakly similar to heterogeneous nuclear ribonucleoprotein K [Rattus norvegicus] [R.norvegicus], heterogeneous nuclear ribonucleoprotein K, poly(rC) binding protein 3, poly(rC) binding protein 4	
761	10108	A1007857	u, v	HGF-regulated tyrosine kinase substrate, hepatocyte growth factor-regulated tyrosine kinase substrate	ESTs, Weakly similar to HGF-regulated tyrosine kinase substrate [Mus musculus] [M.musculus], HGF-regulated tyrosine kinase substrate, RIKEN cDNA 1700013B03 gene, WD40- and FYVE-domain containing protein 2, hepatocyte growth factor-regulated tyrosine kinase substrate, myotubularin related protein 3, phosphoinositide-binding protein SR1, target of myb1 homolog (chicken), zinc finger protein, subfamily 2A (FYVE domain containing), 1	
1942	1375	NM_017122	n, o	hippocalcin	ESTs, Highly similar to HIPPOCALCIN [M.musculus], hippocalcin	
369	17345	AA892014	hh	HLA-B associated transcript 1, HLA-B-associated transcript 1A	ESTs, Highly similar to S33681 translation initiation factor eIF-4A, [H.sapiens], ESTs, Weakly similar to A42811 nuclear RNA helicase (DEAD family) homolog - rat [R.norvegicus], RIKEN cDNA 2610307C23 gene, hypothetical protein MGC6664	
1839	571	NM_012982	cc, dd	homeo box, msh-like 2, msh homeo box homolog 2 (Drosophila)	homeo box, msh-like 2, msh homeo box homolog 2 (Drosophila)	
2368	15748	NM_053309	ii	Homer, neuronal immediate early gene, 2, homer, neuronal immediate early gene, 2	Homer, neuronal immediate early gene, 2, homer, neuronal immediate early gene, 1	
1888	22306	NM_013179	aa, bb	hypocretin, hypocretin (orexin) neuropeptide precursor	hypocretin, hypocretin (orexin) neuropeptide precursor	
2188	1146	NM_024359	y, z	hypoxia inducible factor 1, alpha subunit, hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	Mus musculus inhibitory PAS domain protein (lpas) mRNA, complete cds, hypoxia inducible factor 1, alpha subunit, hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor), neuronal PAS domain protein 1, single-minded 1, single-minded 2, single-minded homolog 1 (Drosophila)	

TABLE 3

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atty. Ref. 44921-5090-01-WQI2105485
2302	21772	NM_031624	y, z	immunoglobulin (CD79A) binding protein 1	expressed sequence C81413, immunoglobulin (CD79A) binding protein 1,	
1927	1427	NM_017063	hh	importin beta, karyopherin (importin) beta 1	immunoglobulin (CD79A) binding protein 1b	
1800	10248	NM_012797	b, j, k, s, t, u, j, kk	inhibitor of DNA binding 1, inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	importin beta, karyopherin (importin) beta 1, karyopherin (importin) beta 3	
1857	15253	NM_013058	n, o, s, t	inhibitor of DNA binding 3, inhibitor of DNA binding 3, dominant negative helix-loop-helix protein		
2223	18188	NM_031046	gg	inositol 1,4,5-triphosphate receptor 2, inositol 1,4,5-triphosphate receptor, type 2	ESTs, Highly similar to IP3R MOUSE INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR [M.musculus], ESTs, Moderately similar to IP3R MOUSE INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR [M.musculus], ESTs, Weakly similar to IP3R MOUSE INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR [M.musculus], inositol 1,4,5-triphosphate receptor 1, inositol 1,4,5-triphosphate receptor 2, inositol 1,4,5-triphosphate receptor 5, inositol 1,4,5-triphosphate receptor, type 2, ryanodine receptor 2 (cardiac), ryanodine receptor 2, cardiac, ryanodine receptor 3	
260	23336	AA859981	ee, ff, jj, kk	inositol(myo)-1(or 4)-monophosphatase 2	ESTs, Moderately similar to A Chain A, Inositol Monophosphatase [H.sapiens], RIKEN cDNA 2900059K10 gene, inositol(myo)-1(or 4)-monophosphatase 1, inositol(myo)-1(or 4)-monophosphatase 2	
2363	25072	NM_052807	j, k	insulin-like growth factor 1 receptor, insulin-like growth factor I receptor	EST, Highly similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR [M.musculus], EST, Moderately similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR [M.musculus], ESTs, Highly similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR [M.musculus], insulin receptor-related receptor, insulin-like growth factor 1 receptor, insulin-like growth factor I receptor	
1754	15098	NM_012588	bb	insulin-like growth factor binding protein 3	insulin-like growth factor binding protein 3	
1356	14989	AI177366	f, g, i, m, kk	integrin beta 1 (fibronectin receptor beta), integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	integrin beta 1 (fibronectin receptor beta), integrin beta 2, integrin beta 7, integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12), integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit), integrin, beta 7	

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SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
					ESTs, Weakly similar to ICA1_HUMAN INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR [H.sapiens], intercellular adhesion molecule, intercellular adhesion molecule 1 (CD54), human rhinovirus receptor, intercellular adhesion molecule 3, intercellular adhesion molecule 5, telencephalin		
1835	2555 NM_012967		a, y, z, kk	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor			
2017	20318 NM_019127		n, o	interferon beta, fibroblast, interferon, beta 1, fibroblast	interferon beta, fibroblast, interferon, beta 1, fibroblast		
2044	17908 NM_019242		a, p, q, y, z, bb, ee, ff	interferon-related developmental regulator 1	ESTs, Weakly similar to IFR1_RAT INTERFERON-RELATED DEVELOPMENTAL REGULATOR 1 (NERVE GROWTH FACTOR-INDUCIBLE PROTEIN PC4) (IRPR) [R.norvegicus], interferon-related developmental regulator 1, interferon-related developmental regulator 2		
2516	657 NM_133380		j, k, y, z	interleukin 4 receptor, interleukin 4 receptor, alpha	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage), interleukin 4 receptor, interleukin 4 receptor, alpha		
1914	6598 NM_017020		j, k	interleukin 6 receptor, interleukin 6 receptor, alpha			
1755	24716 NM_012589		j, k, p, q	interleukin 6, interleukin 6 (interferon, beta 2)	interleukin 6 receptor		
2158	202 NM_022863		h, l	iron responsive element binding protein 2, iron-responsive element binding protein 2			
					ESTs, Highly similar to IDHC_RAT ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC (CDH) (IDP) [R.norvegicus], expressed sequence A1788952, isocitrate dehydrogenase 1 (NADP+), soluble, isocitrate dehydrogenase 2 (NADP+), mitochondrial		
2275	17427 NM_031510		b, u, v	isocitrate dehydrogenase 1 (NADP+), soluble	ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR [H.sapiens], isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase		
1756	4450 NM_012592	c		isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase			
					ESTs, Weakly similar to JC4127 protein-tyrosine kinase (EC 2.7.1.112) - rat [R.norvegicus], Janus kinase 1, Janus kinase 1 (a protein tyrosine kinase), Janus kinase 2, Janus kinase 2 (a protein tyrosine kinase), expressed sequence A1504024, expressed sequence C81284, tyrosine kinase 2		
2276	12580 NM_031514		a, h, i, j, k, y, z	Janus kinase 2, Janus kinase 2 (a protein tyrosine kinase)	ESTs, Weakly similar to JC4127 protein-tyrosine kinase (EC 2.7.1.112) - rat [R.norvegicus], Janus kinase 1, Janus kinase 1 (a protein tyrosine kinase), Janus kinase 2, Janus kinase 2 (a protein tyrosine kinase), expressed sequence A1504024, expressed sequence C81284, tyrosine kinase 2		
2276	12581 NM_031514		y, z, hh	Janus kinase 2, Janus kinase 2 (a protein tyrosine kinase)			

TABLE 3

SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atty. Ref. 44921-5090-01-WO/2105485
2038	2632 NM_019213		cc, dd	jumping translocation breakpoint	ESTs, Highly similar to jumping translocation breakpoint [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to jumping translocation breakpoint [Rattus norvegicus] [R.norvegicus], jumping translocation breakpoint	
2089	22351 NM_021835		ee, ff	Jun oncogene, v-jun sarcoma virus 17 oncogene homolog (avian)	Jun oncogene, v-jun sarcoma virus 17 oncogene homolog (avian)	
2330	15864 NM_031797		r	kangai 1 (suppression of tumorigenicity 6, prostate), kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody (A4))	kangai 1 (suppression of tumorigenicity 6, prostate), kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody (A4)), tetraspan 1	
2390	14380 NM_053536		e, y, z	Kruppel-like factor 15	ESTs, Moderately similar to Kruppel-like factor 9 [Rattus norvegicus] [R.norvegicus], Kruppel-like factor 9, basic transcription element binding protein 1, expressed sequence AL022736	
2489	8641 NM_057211		bb	Kruppel-like factor 9, basic transcription element binding protein 1	lactate dehydrogenase 1, A chain, lactate dehydrogenase A-like, lactate dehydrogenase C	
1915	17807 NM_017025		h, l	lactate dehydrogenase 1, A chain, lactate dehydrogenase A	lactate dehydrogenase 2, B chain, lactate dehydrogenase B	
1757	7125 NM_012595		aa, bb	lamin A, lamin A/C	EST, Weakly similar to 1405340A protein 40kD [M.musculus], EST, Weakly similar to RSP4 MOUSE 40S RIBOSOMAL PROTEIN SA [M.musculus], ESTs, Highly similar to A31233 ribosomal protein RS.40K, cytosolic [H.sapiens], ESTs, Moderately similar to laminin-binding protein [H.sapiens], expressed sequence AL022858, laminin receptor 1 (67kD, ribosomal protein SA)	
1949	24885 NM_017138		h, l, w, x	laminin receptor 1 (67kD, ribosomal protein SA)	EST, Weakly similar to 1405340A protein 40kD [M.musculus], EST, Weakly similar to RSP4 MOUSE 40S RIBOSOMAL PROTEIN SA [M.musculus], ESTs, Highly similar to A31233 ribosomal protein RS.40K, cytosolic [H.sapiens], ESTs, Moderately similar to laminin-binding protein [H.sapiens], expressed sequence AL022858, laminin receptor 1 (67kD, ribosomal protein SA)	
1949	24886 NM_017138		h, l, w, x	laminin receptor 1 (67kD, ribosomal protein SA)	ESTs, Weakly similar to LMB2_HUMAN LAMININ BETA-2 CHAIN PRECURSOR [H.sapiens], Rattus norvegicus laminin-5 alpha 3 chain mRNA, complete cds, expressed sequence AW211941, expressed sequence C80098, hypothetical protein BC018697, laminin B1 subunit 1, laminin, beta 1, laminin, beta 2, laminin, beta 2 (laminin S), laminin, beta 4	
1836	22434 NM_012974		l, m	laminin, beta 2, laminin, beta 2 (laminin S)		



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1836	22435	NM_012974	c	laminin, beta 2, laminin, beta 2 (laminin S)	ESTs, Weakly similar to LMB2_HUMAN LAMININ BETA-2 CHAIN PRECURSOR [H.sapiens], Rattus norvegicus laminin-5 alpha 3 chain mRNA, complete cds, expressed sequence AW211941, expressed sequence C80098, hypothetical protein BC018697, laminin B1 subunit 1, laminin, beta 1, laminin, beta 2, laminin, beta 2 (laminin S), laminin, beta 4	
2335	22321	NM_031832	a, h, l, n, o, x, kk	lectin, galactose binding, soluble 3, lectin, galactoside-binding, soluble, 3 (galectin 3)	EST, Weakly similar to A35820 galectin 3 [H.sapiens], galectin-related inter-fiber protein, lectin, galactoside-binding, soluble, 3 (galectin 3)	
602	22283	AA945172	e	leucine aminopeptidase 3	aminopeptidase-like 1, leucine aminopeptidase 3	
2369	7207	NM_053326	hh	LIM protein (similar to rat protein kinase C-binding enigma), enigma homolog (R. norvegicus)	LIM and senescent cell antigen-like domains 1, LIM and senescent cell antigen-like domains 1-like, LIM protein (similar to rat protein kinase C-binding enigma), RIKEN cDNA 1110003B01 gene, enigma (LIM domain protein), enigma homolog (R. norvegicus), leupaxin	
1781	25563	NM_012732	f, g	lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1	ESTs, Weakly similar to cholesterol esterase (pancreatic), see D3Wox12, D3Wox13, D3Wox26 and D3Mgh25 [Rattus norvegicus] [R. norvegicus], lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1	
1781	16613	NM_012732	g	lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1	ESTs, Weakly similar to cholesterol esterase (pancreatic), see D3Wox12, D3Wox13, D3Wox26 and D3Mgh25 [Rattus norvegicus] [R. norvegicus], lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1	
1758	18387	NM_012598	w, x	lipoprotein lipase	ESTs, Highly similar to JH0790 lipoprotein lipase (EC 3.1.1.34) precursor - rat [R. norvegicus], lipase, endothelial, lipoprotein lipase	
1758	18386	NM_012598	w, x	lipoprotein lipase	ESTs, Highly similar to JH0790 lipoprotein lipase (EC 3.1.1.34) precursor - rat [R. norvegicus], Lipoprotein lipase, lipase, endothelial, lipoprotein lipase	
2375	9352	NM_053347	u, v	LIS1-interacting protein NUDE1, rat homolog, nuclear distribution gene E homolog (Aspergillus)		
217	21713	AA851637	e, r	Lutheran blood group (Auberg b antigen included)	Lutheran blood group (Auberg b antigen included)	
1808	18770	NM_012857	hh	lysosomal membrane glycoprotein 1, lysosomal-associated membrane protein 1	CD68 antigen, ESTs, Weakly similar to LMP1_RAT LYOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 1 PRECURSOR (LAMP-1) (120 KD LYOSOMAL MEMBRANE GLYCOPROTEIN) (LGP-120) (CD107A) [R. norvegicus], chromosome 20 open reading frame 103, lysosomal membrane glycoprotein 1, lysosomal-associated membrane protein 1, lysosomal-associated membrane protein 3	

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1928	6653	NM_017068	d	lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2	CD68 antigen, ESTs, Weakly similar to JC4317 lysosome-associated membrane protein 2 precursor, splice form B [H.sapiens], lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2	
1928	6654	NM_017068	b, v	lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2	CD68 antigen, ESTs, Weakly similar to JC4317 lysosome-associated membrane protein 2 precursor, splice form B [H.sapiens], lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2	
410	12118	AA892775	a, n, x	lysosome, lysosome (renal amyloidosis)	EST, Weakly similar to LYC1_RAT Lysozyme C, type 1 precursor (1,4-beta-N-acetylmuramidase C) [R.norvegicus], RIKEN cDNA 9530003J23 gene, lysozyme, lysozyme (renal amyloidosis), similar to lysozyme C-1 (1,4-beta-N-acetylmuramidase C, EC 3.2.1.17)	
1926	1942	NM_017061	f, ll	lysyl oxidase	ESTs, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE PRECURSOR [H.sapiens], ESTs, Moderately similar to LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus], ESTs, Weakly similar to LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus], lysyl oxidase, lysyl oxidase-like, lysyl oxidase-like 1, lysyl oxidase-like 2	
1926	1943	NM_017061	s, t	lysyl oxidase	ESTs, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE PRECURSOR [H.sapiens], ESTs, Moderately similar to LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus], ESTs, Weakly similar to LYOX_RAT Protein-lysine 6-oxidase precursor (Lysyl oxidase) [R.norvegicus], lysyl oxidase, lysyl oxidase-like, lysyl oxidase-like 1, lysyl oxidase-like 2	
2033	15244	NM_019191	ll	MAD homolog 2 (Drosophila), MAD, mothers against decapentaplegic homolog 2 (Drosophila)	MAD homolog 2 (Drosophila), MAD, mothers against decapentaplegic homolog 2 (Drosophila)	
1809	13151	NM_012862	n, o, ll	matrix Gla protein, matrix gamma-carboxyglutamate (gla) protein	EST, Weakly similar to MGP_HUMAN MATRIX GLA-PROTEIN PRECURSOR [H.sapiens], ESTs, Highly similar to MGP_HUMAN MATRIX GLA-PROTEIN PRECURSOR [H.sapiens], matrix Gla protein, matrix gamma-carboxyglutamate (gla) protein	

TABLE 3

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2615	16675	U17565	r, ii	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae), mini chromosome maintenance deficient 6 (S. cerevisiae)	EST, Weakly similar to MCM5_HUMAN DNA REPLICATION LICENSING FACTOR MCM5 [H.sapiens], ESTs, Weakly similar to MCM6_HUMAN DNA REPLICATION LICENSING FACTOR MCM6 [H.sapiens], MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae), MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae), mini chromosome maintenance deficient 2 (S. cerevisiae), mini chromosome maintenance deficient 5 (S. cerevisiae), mini chromosome maintenance deficient 6 (S. cerevisiae), mini chromosome maintenance deficient 7 (S. cerevisiae)
2675	25737	X70667	l, m	melanocortin 3 receptor	
344	19321	AA891666	cc, dd	melanoma antigen, family D, 1	RIKEN cDNA 1700056A17 gene, RIKEN cDNA 1700080O16 gene, RIKEN cDNA 2410003J06 gene, RIKEN cDNA 3830417A13 gene, melanoma antigen, family D, 1, melanoma antigen, family L, 2
2494	2541	NM_080479	aa, bb	melanoma antigen, family D, 2	RIKEN cDNA 2010107K23 gene, RIKEN cDNA 5730494G16 gene, general transcription factor II H, polypeptide 1 (62kD subunit), melanoma antigen, family B, 3, melanoma antigen, family D, 2, melanoma antigen, family E, 1
1877	5837	NM_013143	cc, dd	meprin 1 alpha, meprin A, alpha (PABA peptide hydrolase)	expressed sequence A1098089, meprin 1 alpha, meprin A, alpha (PABA peptide hydrolase)
1954	17287	NM_017149	ii	mesenchyme homeo box 2 (growth arrest-specific homeo box), mesenchyme homeobox 2	homeo box A11, mesenchyme homeo box 1, mesenchyme homeo box 2 (growth arrest-specific homeo box), mesenchyme homeobox 1, mesenchyme homeobox 2
2550	15189	NM_138826	j, k, y, z, ee, ff, kk	metallothionein 1, metallothionein 1A (functional)	EST, Moderately similar to Cd-7 Metallothionein-2 [H.sapiens], EST, Moderately similar to SMHU1E metallothionein 1E [H.sapiens], ESTs, Moderately similar to MT1_RAT METALLOTHIONEIN-I (MT-I) [R.norvegicus], metallothionein 1, metallothionein 4, metallothionein IV
2550	15190	NM_138826	j, k, y, z, ii	metallothionein 1, metallothionein 1A (functional)	EST, Moderately similar to Cd-7 Metallothionein-2 [H.sapiens], EST, Moderately similar to SMHU1E metallothionein 1E [H.sapiens], ESTs, Moderately similar to MT1_RAT METALLOTHIONEIN-I (MT-I) [R.norvegicus], metallothionein 1, metallothionein 4, metallothionein IV

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
					ESTs, Highly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus], KIAA1266 protein, KIAA1610 protein, metastasis associated 1, metastasis associated 1-like 1, metastasis associated 3, metastasis-associated 1-like 1	
2142	20762	NM_022588	r, s, t	metastasis associated 1		
1970	13938	NM_017212	jj, kk	microtubule-associated protein tau		
1970	13940	NM_017212	a	microtubule-associated protein tau		
2510	17564	NM_133283	hh	mitogen activated protein kinase kinase 2, mitogen-activated protein kinase kinase 2		
2300	14957	NM_031622	f	mitogen-activated protein kinase 6	ESTs, Weakly similar to B40033 protein kinase (EC 2.7.1.37) ERK3 - rat [R.norvegicus], mitogen-activated protein kinase 4, mitogen-activated protein kinase 6	
					ESTs, Highly similar to M3K3 MOUSE MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 3 [M.musculus], ESTs, Moderately similar to S12207 hypothetical protein [M.musculus], ESTs, Weakly similar to M3K3_HUMAN MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 [H.sapiens], hypothetical protein FLJ23074, mitogen activated protein kinase kinase 1, mitogen activated protein kinase kinase kinase 2, mitogen activated protein kinase kinase 3, mitogen-activated protein kinase kinase kinase 3	
536	16499	AA925300	p, ee, ff, gg	mitogen-activated protein kinase kinase kinase 3		
2156	58	NM_022715	u, v	Mitral valve prolapse, familial, major vault protein		
2036	21508	NM_019208	ii	multiple endocrine neoplasia 1, multiple endocrine neoplasia I	multiple endocrine neoplasia 1, multiple endocrine neoplasia I	
1152	15291	A111401	hh	multiple inositol polyphosphate histidine phosphatase 1, multiple inositol polyphosphate histidine phosphatase, 1		
					ESTs, Highly similar to multiple PDZ domain protein [Mus musculus] [M.musculus], ESTs, Weakly similar to T30259 multiple PDZ domain protein - mouse [M.musculus] ESTs, Weakly similar to T46612 multi PDZ domain protein 1 - rat [R.norvegicus], Homo sapiens cDNA FLJ25282 fis, clone STM06685, highly similar to Rattus norvegicus mRNA for multi PDZ domain protein, RIKEN cDNA 2810455B10 gene, channel-interacting PDZ domain protein, multiple PDZ domain protein	
2034	21421	NM_019196	ll	multiple PDZ domain protein		
2306	17448	NM_031668	h, l	MYB binding protein (P160) 1a		

TABLE 3

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1759	2628	NM_012603	a, p, q, y, z a, j, k, p, q, y, z, ee, ff, kk	myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog (avian)	myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog (avian)
1759	2629	NM_012603		myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog (avian)	myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog (avian)
1978	1498	NM_017239	d	myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)	EST, Weakly similar to MYH6_RAT Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [H.sapiens], KIAA1000 protein, myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 7, cardiac muscle, beta EST, Highly similar to MYH7_RAT Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYHB_MOUSE MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) [M.musculus], ESTs, Weakly similar to PCNT MOUSE PERICENTRIN [M.musculus], RIKEN cDNA 4932408L24 gene, myosin heavy chain, cardiac muscle, adult, myosin heavy chain-like, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 7, cardiac muscle, beta EST, Highly similar to MYH7_RAT Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYHB_MOUSE MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) [M.musculus], ESTs, Weakly similar to PCNT MOUSE PERICENTRIN [M.musculus], RIKEN cDNA 4932408L24 gene, myosin heavy chain, cardiac muscle, adult, myosin heavy chain-like, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 7, cardiac muscle, beta
1979	20482	NM_017240	c, g	myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1), myosin, heavy polypeptide 7, cardiac muscle, beta	EST, Highly similar to MYH7_RAT Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYHB_MOUSE MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) [M.musculus], ESTs, Weakly similar to PCNT MOUSE PERICENTRIN [M.musculus], RIKEN cDNA 4932408L24 gene, myosin heavy chain, cardiac muscle, adult, myosin heavy chain-like, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 7, cardiac muscle, beta
1979	20483	NM_017240	d	myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1), myosin, heavy polypeptide 7, cardiac muscle, beta	EST, Highly similar to MYH7_RAT Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYHB_MOUSE MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) [M.musculus], ESTs, Weakly similar to PCNT MOUSE PERICENTRIN [M.musculus], RIKEN cDNA 4932408L24 gene, myosin heavy chain, cardiac muscle, adult, myosin heavy chain-like, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 7, cardiac muscle, beta

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1979	20484	NM_017240	e	myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1), myosin, heavy polypeptide 7, cardiac muscle, beta	EST, Highly similar to MYH7_RAT Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYHB_MOUSE MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) [M.musculus], ESTs, Weakly similar to PCNT MOUSE PERICENTRIN [M.musculus], RIKEN cDNA 4932408L24 gene, myosin heavy chain, cardiac muscle, adult, myosin heavy chain-like, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 7, cardiac muscle, beta	
1978	1497	NM_017239	d	myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1), myosin, heavy polypeptide 7, cardiac muscle, beta	EST, Weakly similar to MYH6_RAT Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha) [R.norvegicus], ESTs, Moderately similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [M.musculus], ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM [H.sapiens], KIAA1000 protein, myosin heavy chain, cardiac muscle, adult, myosin, heavy polypeptide 2, skeletal muscle, adult, myosin, heavy polypeptide 4, skeletal muscle, myosin, heavy polypeptide 7, cardiac muscle, beta	
2463	17653	NM_053986	cc, dd	myosin IB	EST, Highly similar to MY1A_RAT Myosin IA (Myosin I alpha) (MMI-alpha) (MMIa) (Myosin heavy chain myr 1) [R.norvegicus], EST, Weakly similar to MYOSIN I ALPHA [M.musculus], Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010010B23:myosin, heavy polypeptide-like (110kD), full insert sequence, myosin IB	
470	24329	AA899253	aa, bb	myristoylated alanine rich protein kinase C substrate, myristoylated alanine-rich protein kinase C substrate	Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730519L10:myristoylated alanine rich protein kinase C substrate, full insert sequence, myristoylated alanine rich protein kinase C substrate, myristoylated alanine-rich protein kinase C substrate	
2041	20938	NM_019223	hh	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase), NADH dehydrogenase Fe-S protein 6	ESTs, Highly similar to NUMM_MOUSE NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT [M.musculus], NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase)	
2282	18389	NM_031545	a, d, y, ee, ff	natriuretic peptide precursor B, natriuretic peptide precursor type B	EST, Moderately similar to ANFB_MOUSE BRAIN NATRIURETIC PEPTIDE PRECURSOR [M.musculus], natriuretic peptide precursor B, natriuretic peptide precursor type B	

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1762	638	NM_012613	aa, bb	natriuretic peptide receptor 1, natriuretic peptide receptor A (atrionatriuretic peptide receptor A)	ESTs, Weakly similar to ATRIAL NATRIURETIC PEPTIDE RECEPTOR A PRECURSOR [M.musculus], Mus musculus, Similar to natriuretic peptide receptor 2, clone IMAGE:5052434, mRNA, partial cds, natriuretic peptide receptor 1, natriuretic peptide receptor A (atrionatriuretic peptide receptor A)	
1761	1298	NM_012610	d	nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16)	Mus musculus, clone IMAGE:5097359, mRNA, partial cds, nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16), p75-like apoptosis-inducing death domain protein PLAIDD	
1761	1299	NM_012610	cc, dd	nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16)	Mus musculus, clone IMAGE:5097359, mRNA, partial cds, nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16), p75-like apoptosis-inducing death domain protein PLAIDD	
1945	24522	NM_017130	u, v	neuraminidase 2, sialidase 2 (cytosolic sialidase)	neuraminidase 2, sialidase 2 (cytosolic sialidase)	
2441	1780	NM_053846	u, v	neurexin 2, neurexin II	ESTs, Highly similar to C40228 neurexin II-alpha precursor - rat [R.norvegicus], ESTs, Moderately similar to NX1A_MOUSE_2 [Segment 2 of 2] Neurexin 1-alpha (Neurexin 1-alpha) (Fragments) [M.musculus], ESTs, Weakly similar to NX1A_MOUSE_1 [Segment 1 of 2] Neurexin 1-alpha (Neurexin 1-alpha) (Fragments) [M.musculus], RIKEN cDNA 4933401A11 gene, chondroitin sulfate proteoglycan 4	
2298	19022	NM_031609	s, t, jj, kk	neuroblastoma, suppression of tumorigenicity 1	dante, neuroblastoma, suppression of tumorigenicity 1	
2098	20450	NM_022239	b, l, m, u, v	neuromedin, neuromedin U	neuromedin, neuromedin U	
1763	24506	NM_012614	c	neuropeptide Y	RIKEN cDNA 071005A05 gene, neuropeptide Y	
2047	24849	NM_019248	aa, bb	neurotrophic tyrosine kinase, receptor, type 3	neurotrophic tyrosine kinase, receptor, type 3	
2629	1715	U72660	a, jj, kk	ninjurin 1	ninjurin 1, ninjurin 2	
1649	20127	AJ011116	j, k, n, o	nitric oxide synthase 3 (endothelial cell), nitric oxide synthase 3, endothelial cell	ESTs, Moderately similar to A Chain A, Human Endothelial Nitric Oxide Synthase With Arginine Substrate {SUB 66-492 [H.sapiens], Homo sapiens cDNA FLJ14885 f1s, clone PLACE1003711, nitric oxide synthase 3 (endothelial cell), nitric oxide synthase 3, endothelial cell	
1840	764	NM_012988	ee, ff	nuclear factor I/A	nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)	
743	17963	AB012231	jj, kk	nuclear factor I/B	Nuclear Factor I/A, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)	
1331	24763	AI176488	jj, kk	nuclear factor I/B	Nuclear Factor I/A, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)	

TABLE 3					
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
				nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	
2670	25090	X63594	j, k		
2058	24674	NM_019328	j, k	nuclear receptor subfamily 4, group A, member 2	nuclear receptor subfamily 4, group A, member 2
2303	567	NM_031628	p, q	nuclear receptor subfamily 4, group A, member 3	nuclear receptor subfamily 4, group A, member 3
755	18731	AF093139	d	nuclear RNA export factor 1, nuclear RNA export factor 1 homolog (S. cerevisiae)	
299	4339	AA875121	jj, kk	nuclear transcription factor Y, gamma, nuclear transcription factor-Y gamma	
1810	4338	NM_012866	u, v	nuclear transcription factor Y, gamma, nuclear transcription factor-Y gamma	
1841	17394	NM_012992	hh, kk	nucleophosmin (nucleolar phosphoprotein B23, numatrin), nucleophosmin 1	ESTs, Highly similar to A32915 nucleophosmin [H.sapiens], nucleophosmin 1
					ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], SET
752	16006	AF062594	gg	nucleosome assembly protein 1-like 1	ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], SET translocation, SET translocation (myeloid leukemia-associated), nucleosome assembly protein 1-like 1
					ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], SET
752	16007	AF062594	hh	nucleosome assembly protein 1-like 1	translocation, SET translocation (myeloid leukemia-associated), nucleosome assembly protein 1-like 1
					ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], SET
926	7665	A1030668	a	nucleosome assembly protein 1-like 1	translocation, SET translocation (myeloid leukemia-associated), nucleosome assembly protein 1-like 1
1862	13283	NM_013078	b	ornithine carbamoyltransferase, ornithine transcarbamylase	ornithine carbamoyltransferase, ornithine transcarbamylase
2141	21062	NM_022585	gg	ornithine decarboxylase antizyme inhibitor	ESTs, Weakly similar to ODC1_MOUSE Ornithine decarboxylase antizyme inhibitor [M.musculus], ornithine decarboxylase antizyme inhibitor
2141	21063	NM_022585	f, y, z	ornithine decarboxylase antizyme inhibitor	ESTs, Weakly similar to ODC1_MOUSE Ornithine decarboxylase antizyme inhibitor [M.musculus], ornithine decarboxylase antizyme inhibitor
2333	15840	NM_031817	h, l	osteomodulin	osteoglycin, osteomodulin



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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2515	4318	NM_133306	p, q	oxidised low density lipoprotein (lectin-like) receptor 1, oxidized low density lipoprotein (lectin-like) receptor 1	ESTs, Weakly similar to JE0111 lectin-like oxidized LDL receptor - mouse [M.musculus], Mus musculus NKR1F mRNA, complete cds, killer cell lectin-like receptor subfamily B member 1A, killer cell lectin-like receptor subfamily B member 1B, killer cell lectin-like receptor subfamily B member 1D, oxidised low density lipoprotein (lectin-like) receptor 1, oxidized low density lipoprotein (lectin-like) receptor 1	
1690	20549	K01701	b	oxytocin, oxytocin, prepro- (neurophysin I)	ESTs, Moderately similar to NEU1 MOUSE OXYTOCIN-NEUROPHYSIN 1 PRECURSOR [M.musculus], oxytocin, oxytocin, prepro- (neurophysin I)	
2289	1918	NM_031576	gg	P450 (cytochrome) oxidoreductase		
2289	1920	NM_031576	s	P450 (cytochrome) oxidoreductase		
2289	1921	NM_031576	j, k, s, t	P450 (cytochrome) oxidoreductase		
1843	24263	NM_012999	f	paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6	EST, Highly similar to I53282 gene PACE4 protein - rat [R.norvegicus], RIKEN cDNA A930029K19 gene, paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6	
1843	24264	NM_012999	g	paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6	EST, Highly similar to I53282 gene PACE4 protein - rat [R.norvegicus], RIKEN cDNA A930029K19 gene, paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6	
2046	11218	NM_019247	b, u, v	paired-like homeodomain transcription factor 3	ESTs, Weakly similar to PIX3_RAT Pituitary homeobox 3 (Homeobox protein PTX3) [R.norvegicus], RIKEN cDNA 1600026O01 gene, diencephalon/mesencephalon-expressed brain homeobox 1, newborn ovary homeobox gene, paired-like homeodomain transcription factor 3	
2066	18819	NM_019367	l, m	palmitoyl-protein thioesterase 2	palmitoyl-protein thioesterase 2	
2066	18820	NM_019367	s, t	palmitoyl-protein thioesterase 2	palmitoyl-protein thioesterase 2	
2014	1581	NM_017365	l, p, q, s, t	PDZ and LIM domain 1 (elfin)	EST, Moderately similar to CL36_HUMAN LIM DOMAIN PROTEIN CLP-36 [H.sapiens], ESTs, Weakly similar to PDL1_RAT PDZ and LIM domain protein 1 (LIM domain protein CLP-36) (C-terminal LIM domain protein 1) (Elfin) [R.norvegicus], Mus musculus, clone MGC:37634 IMAGE:4990983, mRNA, complete cds, PDZ and LIM domain 1 (elfin), PDZ and LIM domain 3, Rattus norvegicus LIM-domain protein LMP-1 mRNA, complete cds, actinin alpha 2 associated LIM protein	
1974	18148	NM_017226	n, o	peptidyl arginine deiminase, type II	ESTs, Highly similar to PROTEIN-ARGININE DEIMINASE [M.musculus], peptidyl arginine deiminase, type II	

TABLE 3				Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1974	15108	NM_017226	u, v	peptidyl arginine deiminase, type II	ESTs, Highly similar to PROTEIN-ARGININE DEIMINASE [M.musculus], peptidyl arginine deiminase, type II, ribosomal protein S18
					EST, Moderately similar to A Chain A, Cyclophilin A [H.sapiens], ESTs, Highly similar to CYPH MOUSE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [M.musculus], ESTs, Moderately similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr Cyclosporin [H.sapiens], ESTs, Weakly similar to A Chain A, Cyclophilin A [H.sapiens], ESTs, Weakly similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr Cyclosporin [H.sapiens], ESTs, Weakly similar to CYPH_RAT Peptidyl-prolyl cis-trans isomerase A (PPIase) (Cyclophilin A) (Cyclosporin A-binding protein) (P31) [R.norvegicus], RIKEN cDNA 2510026K04 gene, expressed sequence A1256741, expressed sequence AW457192, peptidylprolyl isomerase A
1939	4391	NM_017101	s, t	peptidylprolyl isomerase A (cyclophilin A)	EST, Weakly similar to period homolog 2 (Drosophila) [Rattus norvegicus] [R.norvegicus], ESTs, Highly similar to period homolog 2 (Drosophila) [Rattus norvegicus] [R.norvegicus], period homolog 1 (Drosophila), period homolog 2 (Drosophila)
2310	15041	NM_031678	jj, kk	period homolog 2 (Drosophila)	
1917	4500	NM_017037	ii	peripheral myelin protein 22, peripheral myelin protein, 22 kDa	peripheral myelin protein 22, peripheral myelin protein, 22 kDa
745	22567	AB017544	aa	peroxisomal biogenesis factor 14	peroxisomal biogenesis factor 14
1848	20178	NM_013014	w, x	persephin	EST, Weakly similar to persephin [Rattus norvegicus] [R.norvegicus], artemin, persephin
					ESTs, Weakly similar to PTEN MOUSE PROTEIN-TYROSINE PHOSPHATASE PTEN [M.musculus], Mus musculus mRNA for tyrosine phosphatase (Tpte gene), isoform A, splice variant A, phosphatase and tensin homolog, phosphatase and tensin homolog (mutated in multiple advanced cancers 1), phosphatase and tensin homolog (mutated in multiple advanced cancers 1), pseudogene 1
2297	11296	NM_031606	f	phosphatase and tensin homolog, phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	Homo sapiens, clone MGC:22776 IMAGE:4700840, mRNA, complete cds, RIKEN cDNA 1700023A18 gene, RIKEN cDNA 1700081D17 gene, phosphatidylethanolamine binding protein, prostatic binding protein
1977	15598	NM_017236	ii	phosphatidylethanolamine binding protein, prostatic binding protein	

TABLE 3

SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atty. Ref. 44921-5090-01-WO/2105485
1975	24598 NM_017231		hh	phosphatidylinositol transfer protein, phosphatidylinositol transfer protein	EST, Weakly similar to PPI1_RAT PHOSPHATIDYLINOSITOL TRANSFER PROTEIN ALPHA ISOFORM (PTDINS TRANSFER PROTEIN ALPHA) (PTDINSTP) (PI-TP-ALPHA) [R.norvegicus], phosphatidylinositol transfer protein, phosphatidylinositol transfer protein, retinal degeneration B2 homolog (Drosophila) ESTs, Weakly similar to A34671 triacylglycerol lipase [M.musculus], ESTs, Weakly similar to S15893 triacylglycerol lipase [M.musculus], Homo sapiens membrane-bound phosphatidic acid-selective phospholipase A1 mRNA, complete cds, expressed sequence AA988889, lipase, endothelial, pancreatic lipase-related protein 2	
2558	945 NM_138882		j, k, s, t	phosphatidylserine-specific phospholipase A1, phosphatidylserine-specific phospholipase A1alpha		
63	14250 AA799729		j, k	phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila), phosphodiesterase 9A	
1916	14247 NM_017031		h, l	phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila), phosphodiesterase 9A	
2320	1340 NM_031715		jj, kk	phosphofructokinase, muscle	ESTs, Highly similar to phosphofructokinase, muscle; phosphofructokinase-1 A isozyme [Mus musculus] [M.musculus], expressed sequence A1131669, phosphofructokinase, muscle	
1701	12058 L25387		w	phosphofructokinase, platelet	ESTs, Highly similar to K6PP_MOUSE 6-PHOSPHOFRUCTOKINASE, TYPE C (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME C) (PFK-C) [M.musculus], ESTs, Moderately similar to A53047 6-phosphofructokinase [R.norvegicus], ESTs, Weakly similar to JC2055 6-phosphofructokinase [H.sapiens], ESTs, Weakly similar to K6PL_MOUSE 6-PHOSPHOFRUCTOKINASE, LIVER TYPE [M.musculus], phosphofructokinase, platelet	
1701	25377 L25387		hh	phosphofructokinase, platelet		
2365	1311 NM_053291		e	phosphoglycerate kinase 1	ESTs, Highly similar to A33792 phosphoglycerate kinase (EC 2.7.2.3) - rat [R.norvegicus], phosphoglycerate kinase 1, phosphoglycerate kinase 2	
2003	24533 NM_017328		n, o	phosphoglycerate mutase 2, phosphoglycerate mutase 2 (muscle)	EST, Weakly similar to PMGM_MOUSE PHOSPHOGLYCERATE MUTASE, MUSCLE FORM [M.musculus], EST, Weakly similar to PMHUYM phosphoglycerate mutase [H.sapiens], phosphoglycerate mutase 2, phosphoglycerate mutase 2 (muscle)	

TABLE 3

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atty. Ref. 44921-5090-01-WO/2105483
2446	11405	NM_053866	f	phospholipase A2, activating protein, phospholipase A2-activating protein	phospholipase A2, activating protein, phospholipase A2-activating protein	
2528	244	NM_133551	a, j, k, y, z, ee, ff, kk	phospholipase A2, group IVA (cytosolic, calcium-dependent)	ESTs, Highly similar to FGD1_HUMAN PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [H.sapiens], ESTs, Weakly similar to B39898 phospholipase A2 [M.musculus], ESTs, Weakly similar to FGD1 MOUSE PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [M.musculus], ESTs, Weakly similar to FGD1_HUMAN PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [H.sapiens], FGD1 family, member 3, Homo sapiens cDNA FLJ32732 fis, clone TEST1200141, highly similar to Rattus norvegicus actin-filament binding protein Frabin mRNA, Mus musculus actin-binding protein frabin-alpha mRNA, complete cds, RIKEN cDNA 2310026J01 gene, RIKEN cDNA 2610311B01 gene, RIKEN cDNA 5830461L01 gene, facio-genital dysplasia homolog, hypothetical protein FLJ11183, phospholipase A2, group IVA (cytosolic, calcium-dependent), phospholipase A2, group IVB (cytosolic)	
1962	9378	NM_017174	jj, kk	phospholipase A2, group V	phospholipase A2, group V	
2186	20933	NM_024353	h, l	phospholipase C, beta 4	Homo sapiens mRNA; cDNA DKFZp434E235 (from clone DKFZp434E235), phospholipase C, beta 1	
2288	546	NM_031573	h, ii	phosphorylase kinase gamma, phosphorylase kinase, gamma 1 (muscle)	ESTs, Moderately similar to KPBG_HUMAN PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN, SKELETAL MUSCLE ISOFORM [H.sapiens], endoplasmic reticulum (ER) to nucleus signalling 2, phosphorylase kinase gamma, phosphorylase kinase, gamma 1 (muscle)	
92	4832	AA800190	a, e, ii, kk	phosphorylase, glycogen; brain	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase, glycogen; brain	
2595	4834	NM_153821	h, l	phosphorylase, glycogen; brain	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase, glycogen; brain	
2423	13369	NM_053742	n, o	phosphatidylinositol transfer protein, beta	ESTs, Highly similar to PPI2_HUMAN PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM [H.sapiens], phosphatidylinositol transfer protein, beta	
872	1332	A013222	e	platelet derived growth factor, alpha, platelet-derived growth factor alpha polypeptide	platelet derived growth factor, alpha, platelet-derived growth factor alpha polypeptide	
2074	15911	NM_019907	cc, dd	postsynaptic protein CRIPT, postsynaptic protein CRIPT		
1995	82	NM_017297	ii	potassium inwardly-rectifying channel, subfamily J, member 5	potassium inwardly-rectifying channel, subfamily J, member 5	

TABLE 3					Att. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1938	15517	NM_017099	c	potassium inwardly-rectifying channel, subfamily J, member 8	potassium inwardly-rectifying channel, subfamily J, member 8	
1997	1028	NM_017304	ii	potassium voltage-gated channel, shaker-related subfamily, beta member 2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	
1091	13267	A1101847	h, l	potassium voltage-gated channel, shaker-related subfamily, member 5	potassium voltage-gated channel, shaker-related subfamily, member 5	
1940	15776	NM_017108	u, v	potassium voltage-gated channel, subfamily H (eag-related), member 3	RIKEN cDNA C030044P22 gene, expressed sequence AU019351, potassium voltage-gated channel, subfamily H (eag-related), member 3	
1982	16601	NM_017252	s, t	POU domain, class 3, transcription factor 4	POU domain, class 3, transcription factor 4	
2524	2788	NM_133528	s, t	preimplantation protein 3	preimplantation protein 3	
					ESTs, Weakly similar to Ser/Arg-related nuclear matrix protein; plenty-of-prolines-101; serine/arginine repetitive matrix protein 1 [Mus musculus] [M.musculus], Mus musculus, Similar to hypothetical protein MGC13125, clone MGC:38070 IMAGE:5252666, mRNA, complete cds, PRKC, apoptosis, WT1, regulator, expressed sequence A1480556, glucocorticoid-induced gene 1, serine/arginine repetitive matrix 1	
2361	23895	NM_033485	aa	PRKC, apoptosis, WT1, regulator		
					EST, Weakly similar to PCO1_HUMAN PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PCO1_RAT Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COOH-terminal proteinase enhancer) (Type 1 procollagen C-proteinase enhancer protein) [R.norvegicus], expressed sequence A1043106, membrane frizzled-related protein, procollagen C-endopeptidase enhancer, procollagen C-endopeptidase enhancer 2, procollagen C-proteinase enhancer protein	
2043	15503	NM_019237	n, o	procollagen C-endopeptidase enhancer, procollagen C-proteinase enhancer protein		
				procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55), prolyl 4-hydroxylase, beta polypeptide		
1842	19393	NM_012998	h, l	prodynorphin		
2068	20298	NM_019374	l, m	progesterone receptor membrane component 1		
2088	17936	NM_021766	d, r, gg	progesterone receptor membrane component 1		
2107	11454	NM_022381	d, l, m, n, o, s, t	proliferating cell nuclear antigen		

TABLE 3					Att. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2107	11455	NM_022381	s	proliferating cell nuclear antigen	proliferating cell nuclear antigen	
1847	23545	NM_013013	l, m	prosaposin, prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)		
1776	501	NM_012704	ii	prostaglandin E receptor 3 (subtype EP3)		
1776	503	NM_012704	n, o	prostaglandin E receptor 3 (subtype EP3)		
2045	21108	NM_019243	f	prostaglandin F2 receptor negative regulator	RIKEN cDNA 4833439O17 gene, immunoglobulin superfamily, member 2, immunoglobulin superfamily, member 3, immunoglobulin superfamily, member 8, prostaglandin F2 receptor negative regulator	
2285	692	NM_031557	s, t, ll	prostaglandin I2 (prostacyclin) synthase	EST, Highly similar to PTGI-RAT Prostacyclin synthase (Prostaglandin I2 synthase) [R.norvegicus], cytochrome P450, subfamily VIII B (sterol 12-alpha-hydroxylase), polypeptide 1, prostaglandin I2 (prostacyclin) synthase	
1976	20193	NM_017232	p, q	prostaglandin-endoperoxide synthase 2, prostaglandin G/H synthase and cyclooxygenase	prostaglandin-endoperoxide synthase 2, prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	
1991	15142	NM_017278	l, m	proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) subunit, alpha type, 1	proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) subunit, alpha type, 1	
190	18673	AA849028	t	proteasome (prosome, macropain) subunit, alpha type 3, proteasome (prosome, macropain) subunit, alpha type, 3	EST, Weakly similar to SNHUC8 multicatalytic endopeptidase complex [H.sapiens], ESTs, Highly similar to PRC8 MOUSE PROTEASOME COMPONENT C8 [M.musculus], ESTs, Weakly similar to PRC8 MOUSE PROTEASOME COMPONENT C8 [M.musculus], proteasome (prosome, macropain) subunit, alpha type 3, proteasome (prosome, macropain) subunit, alpha type, 3	
1992	15538	NM_017283	r	proteasome (prosome, macropain) subunit, alpha type 6, proteasome (prosome, macropain) subunit, alpha type, 6	ESTs, Highly similar to S30274 multicatalytic endopeptidase complex [H.sapiens], ESTs, Weakly similar to JX0230 multicatalytic endopeptidase complex (EC 3.4.99.46) iota chain - rat [R.norvegicus], proteasome (prosome, macropain) subunit, alpha type 6	

TABLE 3

Atty. Ref. 44921-5090-01-WO/2105485				Human Homologous Sequence Cluster Title	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	
					EST, Highly similar to PSA7_HUMAN PROTEASOME SUBUNIT ALPHA TYPE 7 (PROTEASOME SUBUNIT RC6-1) (PROTEASOME SUBUNIT XAPC7) [H.sapiens], EST, Highly similar to S60038 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha chain RC6-I - rat [R.norvegicus], Homo sapiens, similar to Proteasome subunit alpha type 7 (Proteasome subunit RC6-1), clone MGC:26605 IMAGE:4829939, mRNA, complete cds, RIKEN cDNA 2410072D24 gene, proteasome (prosome, macropain) subunit, alpha type 7, proteasome (prosome, macropain) subunit, alpha type, 7
1662	9029	D30804	hh	proteasome (prosome, macropain) subunit, alpha type 7, proteasome (prosome, macropain) subunit, alpha type, 7	
1777	4003	NM_012708	e	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2), proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2)	
2346	17601	NM_031976	a, jj, kk	protein kinase, AMP-activated, beta 1 non-catalytic subunit	expressed sequence AW049591, protein kinase, AMP-activated, beta 1 non-catalytic subunit
1859	21287	NM_013065	l, m	protein phosphatase 1, catalytic subunit, beta isoform	protein phosphatase 1, catalytic subunit, beta isoform
2503	9633	NM_130403	jj, kk	protein phosphatase 1, regulatory (inhibitor) subunit 14A	RIKEN cDNA 20107K19 gene, RIKEN cDNA 4933415F23 gene, protein phosphatase 1, regulatory (inhibitor) subunit 14A, protein phosphatase 1, regulatory (inhibitor) subunit 14B, protein phosphatase 1, regulatory (inhibitor) subunit 14C, protein phosphatase 1, regulatory (inhibitor) subunit 14c
2148	24564	NM_022676	f	protein phosphatase 1, regulatory (inhibitor) subunit 1A	EST, Weakly similar to IPPT_HUMAN PROTEIN PHOSPHATASE INHIBITOR 1 [H.sapiens], ESTs, Moderately similar to PROTEIN PHOSPHATASE INHIBITOR 1 [R.norvegicus], Mus musculus, clone MGC:18770 IMAGE:4164563, mRNA, complete cds, RIKEN cDNA 4930565M23 gene, protein phosphatase 1 regulatory subunit 1A, protein phosphatase 1, regulatory (inhibitor) subunit 1A
1918	3203	NM_017039	c	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform, protein phosphatase 2a, catalytic subunit, alpha isoform	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform, protein phosphatase 2a, catalytic subunit, alpha isoform
1919	24597	NM_017040	b, l, m, u, v	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform, protein phosphatase 2a, catalytic subunit, beta isoform	Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600017J22:protein phosphatase 2a, catalytic subunit, beta isoform, full insert sequence, protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform, protein phosphatase 2a, catalytic subunit, beta isoform

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2292	24219	NM_031579	d, p, q, y, z, kk	protein tyrosine phosphatase 4a1, protein tyrosine phosphatase type IVA, member 1	protein tyrosine phosphatase 4a1, protein tyrosine phosphatase 4a3, protein tyrosine phosphatase type IVA, member 1, protein tyrosine phosphatase type IVA, member 3	
1767	1841	NM_012637	d, ji, kk	protein tyrosine phosphatase, non-receptor type 1	EST, Moderately similar to A34845 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1B - rat [R.norvegicus], ESTs, Moderately similar to PTN1_HUMAN PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1 [H.sapiens], protein tyrosine phosphatase, non-receptor type 1	
1767	1844	NM_012637	p, q, y, z	protein tyrosine phosphatase, non-receptor type 1	EST, Moderately similar to A34845 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1B - rat [R.norvegicus], ESTs, Moderately similar to PTN1_HUMAN PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1 [H.sapiens], protein tyrosine phosphatase, non-receptor type 1	
2021	14973	NM_019140	aa	protein tyrosine phosphatase, receptor type, D	ESTs, Weakly similar to 2103274A receptor type protein Tyr phosphatase [M.musculus], RIKEN cDNA 1600019004 gene, expressed sequence AU040377, protein tyrosine phosphatase, receptor type, S	
2085	22916	NM_021740	ii	prothymosin alpha, prothymosin, alpha (gene sequence 28)	ESTs, Highly similar to THYA_HUMAN PROTHYMOSIN ALPHA [H.sapiens], RIKEN cDNA 2610009E16 gene, prothymosin alpha, prothymosin, alpha (gene sequence 28)	
1510	4716	AI232313	c, r	purinergic receptor P2X, ligand-gated ion channel 4, purinergic receptor P2X, ligand-gated ion channel, 4	purinergic receptor P2X, ligand-gated ion channel 4, purinergic receptor P2X, ligand-gated ion channel, 4	
2499	363	NM_080780	d, e, p, q, ee, ff	purinergic receptor P2X, ligand-gated ion channel, 5	purinergic receptor P2X, ligand-gated ion channel, 5	
1983	1496	NM_017255	aa, bb	purinergic receptor P2Y, G-protein coupled 2, purinergic receptor P2Y, G-protein coupled, 2	G protein-coupled receptor 31, Mus musculus, clone MGC:28142 IMAGE:3982042, mRNA, complete cds, RIKEN cDNA 2610302J02 gene, RIKEN cDNA 5830408N17 gene, expressed sequence AI662791, purinergic receptor P2Y, G-protein coupled 2, purinergic receptor P2Y, G-protein coupled, 2	
2208	1928	NM_030872	s, t	pyruvate dehydrogenase 2, pyruvate dehydrogenase kinase, isoenzyme 2	Mus musculus, Similar to pyruvate dehydrogenase kinase, isoenzyme 1, clone MGC:28719 IMAGE:4458562, mRNA, complete cds, Mus musculus, Similar to pyruvate dehydrogenase kinase, isoenzyme 3, clone MGC:6383 IMAGE:3500763, mRNA, complete cds, pyruvate dehydrogenase 2, pyruvate dehydrogenase kinase, isoenzyme 2	



TABLE 3

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atty. Ref. 44921-5090-01-WO/2105485
2208	1929	NM_030872	hh	pyruvate dehydrogenase kinase, isoenzyme 2	Mus musculus, Similar to pyruvate dehydrogenase kinase, isoenzyme 1, clone MGC:28719 IMAGE:4458562, mRNA, complete cds, Mus musculus, Similar to pyruvate dehydrogenase kinase, isoenzyme 3, clone MGC:6383 IMAGE:3500763, mRNA, complete cds, pyruvate dehydrogenase 2, pyruvate dehydrogenase kinase, isoenzyme 2	
2012	20417	NM_017359	h, l, hh	RAB10, member RAS oncogene family	ESTs, Weakly similar to RAB8_HUMAN RAS-RELATED PROTEIN RAB-8 [H.sapiens], RAB10, member RAS oncogene family, RAB12, member RAS oncogene family, RAB38, member RAS oncogene family, expressed sequence AA536966, expressed sequence AW107754	
1849	20229	NM_013018	kk	RAB3A, member RAS oncogene family	ESTs, Weakly similar to C34323 GTP-binding protein Rab3A [H.sapiens], RAB3A, member RAS oncogene family	
2231	18307	NM_031091	w, x	RAB3B, member RAS oncogene family	RAB3B, member RAS oncogene family	
2231	18308	NM_031091	w, x	RAB3B, member RAS oncogene family	RAB3B, member RAS oncogene family	
2133	6577	NM_022532	u, v	raf-related oncogene, v-raf murine sarcoma 3611 viral oncogene homolog 1	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200013E08:raf-related oncogene, full insert sequence, expressed sequence AW495444, raf-related oncogene, v-raf murine sarcoma 3611 viral oncogene homolog 1	
2351	21807	NM_032067	gg	Ral-interacting protein 1, ralA binding protein 1	Ral-interacting protein 1, ralA binding protein 1	
2351	21809	NM_032067	ll	Ral-interacting protein 1, ralA binding protein 1	Ral-interacting protein 1, ralA binding protein 1	
1661	25278	D30734	gg	RAS p21 protein activator 2		
1547	22152	A1234822	j, k	RAS, dexamethasone-induced 1	Mus musculus small GTP-binding tumor suppressor 1 (Gbit1) mRNA, complete cds, Mus musculus, Similar to RAP1A, member of RAS oncogene family, clone MGC:18653 IMAGE:3600519, mRNA, complete cds, RAP2B, member of RAS oncogene family, RAS, dexamethasone-induced 1, RIKEN cDNA 1110065D03 gene, RIKEN cDNA 2010200P20 gene, RIKEN cDNA 5830461H18 gene, rap2A-like protein, ras homolog gene family, member I	
1898	23362	NM_013216	e	RAS-homolog enriched in brain, Ras homolog enriched in brain 2	ESTs, Weakly similar to RALA MOUSE RAS-RELATED PROTEIN RAL-A [M.musculus], RAS-homolog enriched in brain, RIKEN cDNA 1810036J22 gene, Ras homolog enriched in brain 2, ras-like protein VTS58635	
2373	1609	NM_053338	i, p, q, y, z	Ras-related associated with diabetes	ESTs, Weakly similar to Ras-related associated with diabetes [Rattus norvegicus] [R.norvegicus], GTP binding protein (gene overexpressed in skeletal muscle), GTP binding protein overexpressed in skeletal muscle, Ras-related associated with diabetes, rad and gem related GTP binding protein	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2305	16062	NM_031646	n, o	receptor (calcitonin) activity modifying protein 2	receptor (calcitonin) activity modifying protein 2	
2062	2088	NM_019341	aa, bb	regulator of G-protein signalling 5	regulator of G-protein signalling 5	
1947	20916	NM_017132	d	reticulocalbin 2, reticulocalbin 2, EF-hand calcium binding domain	reticulocalbin 2, EF-hand calcium binding domain	regulator of G-protein signalling 5, regulator of G-protein signalling 5
1658	17264	D25233	d	retinoblastoma 1, retinoblastoma 1 (including osteosarcoma)	retinoblastoma 1, retinoblastoma 1 (including osteosarcoma)	ESTs, Weakly similar to I56519 tapoxin-associated calcium binding protein-49 precursor - rat [R.norvegicus], calumenin, reticulocalbin, reticulocalbin 2, reticulocalbin 2, EF-hand calcium binding domain
1419	1377	A122715	a, ee, ff	retinoblastoma-like 2, retinoblastoma-like 2 (p130)	retinoblastoma-like 2, retinoblastoma-like 2 (p130)	EST, Moderately similar to RETINOBLASTOMA-ASSOCIATED PROTEIN [M.musculus], ESTs, Highly similar to RB MOUSE RETINOBLASTOMA-ASSOCIATED PROTEIN [M.musculus], retinoblastoma 1, retinoblastoma 1 (including osteosarcoma)
2233	1376	NM_031094	ii	retinoblastoma-like 2, retinoblastoma-like 2 (p130)	retinoblastoma-like 2, retinoblastoma-like 2 (p130)	Mus musculus 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700054A06:retinoblastoma-like 1 (p107), full insert sequence, retinoblastoma-like 1 (p107), retinoblastoma-like 2, retinoblastoma-like 2 (p130)
1782	23806	NM_012733	j, k	retinol binding protein 1, cellular	retinol binding protein 1, cellular	Mus musculus 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700054A06:retinoblastoma-like 1 (p107), full insert sequence, retinoblastoma-like 1 (p107), retinoblastoma-like 2, retinoblastoma-like 2 (p130)
1850	1338	NM_013022	r	Rho-associated coiled-coil forming kinase 2, Rho-associated, coiled-coil containing protein kinase 2	Rho-associated coiled-coil forming kinase 2, Rho-associated, coiled-coil containing protein kinase 2, expressed sequence AU014939	ESTs, Weakly similar to RET1_RAT Retinol-binding protein 1, cellular (Cellular retinol-binding protein) (CRBP) [R.norvegicus], retinoid binding protein 7, retinol binding protein 1, cellular, retinol binding protein 5, cellular, retinol binding protein 7, cellular
2314	21575	NM_031698	w, x	ribophorin II	ribophorin II	Rho-associated coiled-coil forming kinase 2, Rho-associated, coiled-coil containing protein kinase 2, expressed sequence AU014939
2227	11849	NM_031065	h, i, n, o	ribosomal protein L10A, ribosomal protein L10a	ribosomal protein L10A, ribosomal protein L10a	EST, Moderately similar to RIB2_HUMAN DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KDA SUBUNIT PRECURSOR [H.sapiens], ESTs, Moderately similar to RIB2_HUMAN DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KDA SUBUNIT PRECURSOR [H.sapiens], ribophorin 2, related sequence 1, ribophorin II

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SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2237	23854	NM_031101	f, w, x, ll	ribosomal protein L13	EST, Moderately similar to JC2368 ribosomal protein L13, cytosolic [validated] - rat [R.norvegicus], EST, Weakly similar to JC2368 ribosomal protein L13, cytosolic [validated] - rat [R.norvegicus], ESTs, Highly similar to ribosomal protein L13; 60S ribosomal protein L13; breast basic conserved protein 1 [Homo sapiens] [H.sapiens], ESTs, Moderately similar to RL13 MOUSE 60S RIBOSOMAL PROTEIN L13 [M.musculus], Homo sapiens cDNA FLJ30941 fis, clone FEBRA2007458, Human RPL13-2 pseudogene mRNA, complete cds, ribosomal protein L13	
2238	20462	NM_031102	h, l	ribosomal protein L18	ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L18 [M.musculus], ribosomal protein L18	
2239	16938	NM_031103	g	ribosomal protein L19	EST, Weakly similar to RL19 MOUSE 60S RIBOSOMAL PROTEIN L19 [M.musculus], ESTs, Weakly similar to RL19_HUMAN 60S RIBOSOMAL PROTEIN L1 [M.musculus], ESTs, Weakly similar to RL19_HUMAN 60S ribosomal protein L19 [R.norvegicus], ribosomal protein L19	
2371	14927	NM_053330	e	ribosomal protein L21	EST, Moderately similar to 2113200B ribosomal protein L21 [H.sapiens], EST, Moderately similar to RL21_RAT 60S RIBOSOMAL PROTEIN L21 [R.norvegicus], EST, Weakly similar to 2113200B ribosomal protein L21 [H.sapiens], EST, Weakly similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], EST, Weakly similar to RL21_HUMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], ESTs, Highly similar to 2113200B ribosomal protein L21 [H.sapiens], ESTs, Highly similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], ESTs, Moderately similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], ribosomal protein L21	
2371	14929	NM_053330	h, l	ribosomal protein L21	EST, Moderately similar to 2113200B ribosomal protein L21 [H.sapiens], EST, Moderately similar to RL21_RAT 60S RIBOSOMAL PROTEIN L21 [R.norvegicus], EST, Weakly similar to 2113200B ribosomal protein L21 [H.sapiens], EST, Weakly similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], EST, Weakly similar to RL21_HUMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], ESTs, Highly similar to 2113200B ribosomal protein L21 [H.sapiens], ESTs, Highly similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], ESTs, Moderately similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], ribosomal protein L21	
2658	5667	X58200	h, l, w, x	ribosomal protein L23		

TABLE 3

SEQ ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2125	2696 NM_022515	cc, dd	ribosomal protein L24	Homo sapiens, clone MGC:27044 IMAGE:4793412, mRNA, complete cds, Mus musculus, Similar to 60S ribosomal protein L30 isolog, clone MGC:6735 IMAGE:3590401, mRNA, complete cds, ribosomal protein L24
2125	2697 NM_022515	f, g, gg	ribosomal protein L24	Homo sapiens, clone MGC:27044 IMAGE:4793412, mRNA, complete cds, Mus musculus, Similar to 60S ribosomal protein L30 isolog, clone MGC:6735 IMAGE:3590401, mRNA, complete cds, ribosomal protein L24
2124	3027 NM_022514	w, x	ribosomal protein L27	ribosomal protein L27
2152	17729 NM_022697	f, g, w, x, cc, dd	ribosomal protein L28	ribosomal protein L28
2658	18611 X58200	g	ribosomal protein L29	EST, Moderately similar to RL29_HUMAN 60S RIBOSOMAL PROTEIN L29 [H.sapiens], EST, Moderately similar to RL29_RAT 60S RIBOSOMAL PROTEIN L29 (P23) [R.norvegicus], ESTs, Highly similar to S65784 ribosomal protein L29, cytosolic [H.sapiens], ribosomal protein L29
2078	15335 NM_021264	w	ribosomal protein L35a	EST, Moderately similar to ribosomal protein L36 [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 1110038G14 gene, ribosomal protein L36
2120	4259 NM_022504	f, g	ribosomal protein L36	ESTs, Highly similar to YZA1_HUMAN HYPOTHETICAL PROTEIN [H.sapiens], ribosomal protein L41
2564	15380 NM_139083	u, v, cc, dd	ribosomal protein L41	EST, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [R.norvegicus], EST, Weakly similar to JN0923 ribosomal protein L8, cytosolic [H.sapiens], ESTs, Highly similar to R5RTL8 ribosomal protein L8, cytosolic [validated] - rat [R.norvegicus], ESTs, Highly similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus], ESTs, Moderately similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus], expressed sequence AL024098, ribosomal protein L8
2666	15875 X62145	h, r	ribosomal protein L8	EST, Moderately similar to S65792 ribosomal protein L9, cytosolic [H.sapiens], EST, Weakly similar to RL9_RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L9 [M.musculus], RIKEN cDNA 4930401B11 gene, ribosomal protein L9
2650	18250 X51706	w, x	ribosomal protein L9	ESTs, Moderately similar to RS13_HUMAN 40S RIBOSOMAL PROTEIN S13 [H.sapiens], ribosomal protein S13
2653	20427 X53378	h	ribosomal protein S13	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1955	16953	NM_017151	g	ribosomal protein S15	EST, Moderately similar to R3HU15 ribosomal protein S15, cytosolic [H.sapiens], ESTs, Highly similar to RS15_HUMAN 40S RIBOSOMAL PROTEIN S15 [M.musculus], ribosomal protein S15	
1955	16954	NM_017151	gg	ribosomal protein S15	EST, Moderately similar to R3HU15 ribosomal protein S15, cytosolic [H.sapiens], ESTs, Highly similar to RS15_HUMAN 40S RIBOSOMAL PROTEIN S15 [M.musculus], ribosomal protein S15	
1955	16955	NM_017151	l, m, s, t	ribosomal protein S15	EST, Moderately similar to R3HU15 ribosomal protein S15, cytosolic [H.sapiens], ESTs, Highly similar to RS15_HUMAN 40S RIBOSOMAL PROTEIN S15 [M.musculus], ribosomal protein S15	
2648	15626	X17665	w, x	ribosomal protein S16	EST A1317031, EST, Weakly similar to R3HU16 ribosomal protein S16, cytosolic [H.sapiens], expressed sequence AA420385, ribosomal protein S16	
2651	20872	X51707	l, w, x	ribosomal protein S19	EST, Moderately similar to R3RT19 ribosomal protein S19, cytosolic [validated] - rat [R.norvegicus], EST, Weakly similar to RS19_HUMAN 40S RIBOSOMAL PROTEIN S19 [H.sapiens]	
2492	10498	NM_078617	c, g, w, x	ribosomal protein S23	ESTs, Highly similar to 40S RIBOSOMAL PROTEIN S23 [H.sapiens], ESTs, Weakly similar to ribosomal protein S23 [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to mitochondrial ribosomal protein S12, clone MGC:13892 IMAGE:4209358, mRNA, complete cds, mitochondrial ribosomal protein S12, ribosomal protein S23 ESTs, Highly similar to ribosomal protein S27a [Mus musculus] [M.musculus], ESTs, Highly similar to ubiquitin / ribosomal protein S27a [H.sapiens], ESTs, Weakly similar to ribosomal protein S27a [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to ubiquitin-like 4, clone MGC:19132 IMAGE:4215699, mRNA, complete cds, neural precursor cell expressed, developmentally down-regulated 8, ribosomal protein S27a	
2246	20839	NM_031113	w, x	ribosomal protein S27a	EST, Moderately similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 [M.musculus], ESTs, Weakly similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 [H.sapiens], ribosomal protein S29	
1813	17305	NM_012876	g, hh	ribosomal protein S29	EST, Moderately similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 [M.musculus], ESTs, Weakly similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 [H.sapiens], ribosomal protein S29	
1813	17306	NM_012876	f	ribosomal protein S29	EST, Moderately similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 [M.musculus], ESTs, Weakly similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 [H.sapiens], ribosomal protein S29	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					EST, Moderately similar to RS3_MOUSE 40S ribosomal protein S3 [R.norvegicus], EST, Weakly similar to RS3_MOUSE 40S ribosomal protein S3 [R.norvegicus], ESTs, Highly similar to RS3_MOUSE 40S ribosomal protein S3 [R.norvegicus], ESTs, Moderately similar to RS3_HUMAN 40S RIBOSOMAL PROTEIN S [H.sapiens], ESTs, Weakly similar to RS3_MOUSE 40S RIBOSOMAL PROTEIN S3 [M.musculus], hypothetical protein FLJ11252, hypothetical protein FLJ23059, myo-inositol 1-phosphate synthase A1, ribosomal protein S3
2649	10819	X51536	gg	ribosomal protein S3	
2649	25686	X51536	w, x, hh	ribosomal protein S3	
2659	25702	X58465	g, w, x	ribosomal protein S5	EST, Moderately similar to 2113200E ribosomal protein S5 [H.sapiens], EST, Weakly similar to 2113200E ribosomal protein S5 [H.sapiens], ribosomal protein S5
2659	10109	X58465	g, w, x	ribosomal protein S5	EST, Moderately similar to 2113200E ribosomal protein S5 [H.sapiens], EST, Weakly similar to 2113200E ribosomal protein S5 [H.sapiens], ribosomal protein S5
1957	17104	NM_017160	h, l	ribosomal protein S6	EST, Moderately similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], EST, Moderately similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], EST, Weakly similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], ESTs, Highly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ESTs, Weakly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ESTs, Weakly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ribosomal protein S6
1957	17105	NM_017160	h, l	ribosomal protein S6	EST, Moderately similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], EST, Moderately similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], EST, Weakly similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], ESTs, Highly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ESTs, Weakly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ribosomal protein S6
1957	17106	NM_017160	n, o	ribosomal protein S6	EST, Moderately similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], EST, Moderately similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], EST, Weakly similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], ESTs, Highly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ESTs, Weakly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ribosomal protein S6

TABLE 3						Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
					EST, Moderately similar to JC4388 ribosomal protein S7, cytosolic [H.sapiens], EST, Weakly similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 [M.musculus], EST, Weakly similar to RS7_HUMAN 40S ribosomal protein S7 (S8) [R.norvegicus], ESTs, Highly similar to JC4388 ribosomal protein S7, cytosolic [H.sapiens], ESTs, Highly similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 [H.sapiens], ESTs, Moderately similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 [H.sapiens], ESTs, Moderately similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 [H.sapiens], ribosomal protein S7	
2287	9620	NM_031570	w, x, cc, dd	ribosomal protein S7		
2315	16204	NM_031706	f, g, jj, kk	ribosomal protein S8		
2315	16205	NM_031706	jj, kk	ribosomal protein S8		
64	18061	AA799735	r	RuvB-like 1 (E. coli), RuvB-like protein 1	Homer, neuronal immediate early gene, 1B, homer, neuronal immediate early gene, 1	
2316	18054	NM_031707	f, g, n, o	RuvB-like 1 (E. coli), RuvB-like protein 1	Homer, neuronal immediate early gene, 1B, homer, neuronal immediate early gene, 1	
2316	18057	NM_031707	r	RuvB-like 1 (E. coli), RuvB-like protein 1	Homer, neuronal immediate early gene, 1B, homer, neuronal immediate early gene, 1	
2316	18059	NM_031707	p, q, ee, ff	RuvB-like 1 (E. coli), RuvB-like protein 1	Homer, neuronal immediate early gene, 1B, homer, neuronal immediate early gene, 1	
2247	19040	NM_031114	a, c, h, l, y, ee, ff	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)), S100 calcium binding protein A10 (calpactin)	EST, Moderately similar to S110_RAT Calpactin I light chain (P10 protein) (P11) (Cellular ligand of annexin II) (Nerve growth factor induced protein 42C) [R.norvegicus], S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)), S100 calcium binding protein A10 (calpactin)	
1764	20589	NM_012618	h, l, n, o, w, x	S100 calcium binding protein A4, S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)	S100 calcium binding protein A2, S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)	
2386	16394	NM_053485	h, l, w, x	S100 calcium binding protein A6 (calcyclin)		

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1967	20779	NM_017201	b, l, m	S-adenosylhomocysteine hydrolase	Mus musculus, S-adenosylhomocysteine hydrolase-like 1, clone MGC:18748 IMAGE:4007102, mRNA, complete cds, S-adenosylhomocysteine hydrolase, S-adenosylhomocysteine hydrolase, related sequence 3, expressed sequence AL024110	
2214	15682	NM_031011	n, o	S-adenosylmethionine decarboxylase 1	S-adenosylmethionine decarboxylase 1, S-adenosylmethionine decarboxylase 2	
2214	15683	NM_031011	cc, dd, gg	S-adenosylmethionine decarboxylase 1	S-adenosylmethionine decarboxylase 1, S-adenosylmethionine decarboxylase 2	
1770	16217	NM_012656	c, aa, bb	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	
1770	16218	NM_012656	n, o	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	
1770	16219	NM_012656	r, gg	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	
1770	16220	NM_012656	h, l, aa, bb	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	
1770	16221	NM_012656	d	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)	
1814	23651	NM_012881	h, l, n, o, w, x	secreted phosphoprotein 1, secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1)		
1851	17894	NM_013027	gg	selenoprotein W, 1, selenoprotein W, muscle 1	ESTs, Weakly similar to SELW MOUSE SELENOPROTEIN W [M.musculus], selenoprotein W, 1, selenoprotein W, muscle 1	
1718	21400	M36410	ee, ff, gg	sepiapterin reductase, sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	ESTs, Highly similar to A36024 sepiapterin reductase [EC 1.1.1.153] - rat [R.norvegicus], sepiapterin reductase, sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	
1765	15540	NM_012620	a, kk	serine (or cysteine) proteinase inhibitor, clade E (nexin), plasminogen activator inhibitor type 1, member 1		
1961	17301	NM_017173	c, f, g, j, k, y, z	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, collagen binding protein 1, serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2		



TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2322	15507	NM_031735	u	serine/threonine kinase 3 (STE20 homolog, yeast), serine/threonine kinase 3 (Ste20, yeast homolog)	serine/threonine kinase 24 (STE20 homolog, yeast), serine/threonine kinase 25 (STE20 homolog, yeast), serine/threonine kinase 25 (yeast), serine/threonine kinase 3 (STE20 homolog, yeast), serine/threonine kinase 3 (Ste20, yeast homolog), serine/threonine kinase 4	
2042	20433	NM_019232	p, q, kk	serum/glucocorticoid regulated kinase	EST, Weakly similar to SGK_RAT Serine/threonine-protein kinase Sgk (Serum/glucocorticoid-regulated kinase) [R.norvegicus], Mus musculus, hypothetical protein MGC11287 similar to ribosomal protein S6 kinase, clone MGC:38756 IMAGE:5358742, mRNA, complete cds, RIKEN cDNA 1190006F07 gene, serine/threonine protein kinase CISK, serum/glucocorticoid regulated kinase, serum/glucocorticoid regulated kinase 2, serum/glucocorticoid regulated kinase-like ESTs, Highly similar to SNK_RAT Serine/threonine-protein kinase SNK (Serum inducible kinase) [R.norvegicus], ESTs, Weakly similar to SNK MOUSE SERINE/THREONINE-PROTEIN KINASE SNK [M.musculus], ESTs, Weakly similar to SNK_RAT Serine/threonine-protein kinase SNK (Serum inducible kinase) [R.norvegicus], Homo sapiens cDNA FLJ30246 fis, clone BRACE2002202, weakly similar to SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-), NIMA (never in mitosis gene a)-related expressed kinase 1, NIMA (never in mitosis gene a)-related kinase 4, serum-inducible kinase	
2334	2655	NM_031821	d	serum-inducible kinase	EST, Moderately similar to SSRD_RAT TRANSLOCAN-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR (TRAP-DELTA) (SIGNAL SEQUENCE RECEPTOR DELTA SUBUNIT) (SSR-DELTA) [R.norvegicus], EST, Weakly similar to SSRD_HUMAN TRANSLOCAN-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR [H.sapiens], Mus musculus, clone IMAGE:4038523, mRNA, partial cds, signal sequence receptor, delta, signal sequence receptor, delta (translocon-associated protein delta)	
1966	9124	NM_017199	h, i, hh	signal sequence receptor, delta, signal sequence receptor, delta (translocon-associated protein delta)		

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105486	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2167		15727 NM_022953	u, v	slit homolog 1 (Drosophila)	EST, Highly similar to 142b2b secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment) [M.musculus], ESTs, Weakly similar to hypothetical protein MGC7599; clone MGC:7599 [Mus musculus] [M.musculus], ESTs, Weakly similar to integral membrane glycoprotein [Mus musculus] [M.musculus], ESTs, Weakly similar to ALS MOUSE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to JG0193 G protein-coupled receptor FEX - mouse [M.musculus], ESTs, Weakly similar to Slit-1 protein [H.sapiens], Mus musculus, Similar to leucine-rich repeat-containing 3, clone MGC:30505 IMAGE:4481142, mRNA, complete cds, RIKEN cDNA 9530074E10 gene, slit homolog 1 (Drosophila), slit homolog 2 (Drosophila), slit homolog 3 (Drosophila)	
2277		20448 NM_031530	a, d, z, ee, ff, jj, kk	small inducible cytokine A2, small inducible cytokine A2 (monocyte chemotactic protein 1)	EST, Weakly similar to S07723 immediate-early serum-responsive protein JE precursor - rat [R.norvegicus], expressed sequence A1323594, small inducible cytokine A2, small inducible cytokine A24, small inducible cytokine subfamily A (Cys-Cys), member 24	
2277		20449 NM_031530	a, z, ee, ff, kk	small inducible cytokine A2, small inducible cytokine A2 (monocyte chemotactic protein 1)	EST, Weakly similar to S07723 immediate-early serum-responsive protein JE precursor - rat [R.norvegicus], expressed sequence A1323594, small inducible cytokine A2, small inducible cytokine A24, small inducible cytokine subfamily A (Cys-Cys), member 24	
2545		19077 NM_134455	aa, bb	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin), small inducible cytokine subfamily D, 1	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin), small inducible cytokine subfamily D, 1	
1801		20246 NM_012807	l, m, s	smoothed homolog (Drosophila)	EST, Moderately similar to SMO_HUMAN SMOOTHENED HOMOLOG PRECURSOR [H.sapiens], smoothed homolog (Drosophila)	
1993		20579 NM_017288	aa, bb	sodium channel, voltage-gated, type I, beta polypeptide	Mus musculus brain and heart sodium channel beta 3 subunit mRNA, complete cds, sodium channel beta 3 subunit, sodium channel, voltage-gated, type I, beta polypeptide	

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SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
					ESTs, Weakly similar to EAA3_RAT Excitatory amino acid transporter 3 (Sodium-dependent glutamate/aspartate transporter 3) (Excitatory amino-acid carrier 1) [R.norvegicus], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931413K05:solute carrier family 1, member 1, full insert sequence, Rattus norvegicus mRNA for sodium-dependent neutral amino acid transporter, ASCT2, solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1, solute carrier family 1, member 1, solute carrier family 1, member 7	
1664	21147	D63772	j, k, p	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1, solute carrier family 1, member 1		
2279	1005	NM_031537	l, m	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1		
2331	2114	NM_031798	aa, bb	solute carrier family 12 (sodium/potassium/chloride transporters), member 2, solute carrier family 12, member 2	Mus musculus strain ILS K-Cl cotransporter (Slc12a5) mRNA, complete cds, cation-chloride cotransporter 6, cation-chloride cotransporter 9, cation-chloride cotransporter-interacting protein 1, solute carrier family 12 (sodium/potassium/chloride transporters), member 2, solute carrier family 12, member 2	
1779	20888	NM_012716	c, e	solute carrier family 16 (monocarboxylic acid transporters), member 1	RIKEN cDNA 1110004H10 gene, RIKEN cDNA 1200003C15 gene, solute carrier family 16 (monocarboxylic acid transporters), member 1	
1779	20889	NM_012716	e, aa, bb	solute carrier family 16 (monocarboxylic acid transporters), member 1	RIKEN cDNA 1110004H10 gene, RIKEN cDNA 1200003C15 gene, solute carrier family 16 (monocarboxylic acid transporters), member 1	
				solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 1	solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 1, solute carrier family 19 (thiamine transporter), member 2, solute carrier family 19 (thiamine transporter), member 2, solute carrier family 19, member 3	
1996	23825	NM_017299	cc, dd	solute carrier family 2 (facilitated glucose transporter), member 1	Mus musculus, clone MGC:8298 IMAGE:3593581, mRNA, complete cds, solute carrier family 2 (facilitated glucose transporter), member 1	
2551	16248	NM_138827	y, z	solute carrier family 2 (facilitated glucose transporter), member 1	Mus musculus, clone MGC:8298 IMAGE:3593581, mRNA, complete cds, solute carrier family 2 (facilitated glucose transporter), member 1	
2551	16249	NM_138827	i, k	solute carrier family 2 (facilitated glucose transporter), member 1	Mus musculus, clone MGC:8298 IMAGE:3593581, mRNA, complete cds, solute carrier family 2 (facilitated glucose transporter), member 1	

TABLE 3						Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1973	1510	NM_017224	II	solute carrier family 22 (organic anion transporter), member 6	Homo sapiens, Similar to ust3, clone MGC:23972 IMAGE:4714598, mRNA, complete cds, Mus musculus, Similar to solute carrier family 22 (organic anion transporter), member 7, clone MGC:18877 IMAGE:4236556, mRNA, complete cds, Rattus norvegicus mRNA for organic anion transporter 5, complete cds, expressed sequence A1648912, putative integral membrane transporter UST1r, solute carrier family 22 (organic anion transporter), member 6, solute carrier family 22 (organic cation transporter)-like 2, ust3	
1655	18018	D12771	f, g	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	EST, Moderately similar to S03894 ADP,ATP carrier protein T3 [H.sapiens], EST, Weakly similar to A29132 ADP,ATP carrier protein T2 [H.sapiens], Homo sapiens, clone IMAGE:5215220, mRNA, Mus musculus, Similar to CG4995 gene product, clone MGC:7958 IMAGE:3584570, mRNA, complete cds, RIKEN cDNA 4933440H19 gene, folate transporter/carrier, solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2311	20743	NM_031684	a, x, z, kk	solute carrier family 29 (nucleoside transporters), member 1	ESTs, Weakly similar to solute carrier family 29 (nucleoside transporters), member 1 [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 4933435C21 gene, solute carrier family 29 (nucleoside transporters), member 1	
2052	20734	NM_019283	j, k, t, u, v, ii, kk	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	
2052	20735	NM_019283	j, k, t, y, z, kk	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	
1852	18076	NM_013030	cc, dd	solute carrier family 34 (sodium phosphate), member 1	Rattus norvegicus mRNA for Na+/Pi-co-transporter type 1lc, complete cds, Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, expressed sequence A1649385, solute carrier family 34 (sodium phosphate), member 1	
985	16335	A1045744	b, u, v	solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	ESTs, Moderately similar to B3AT MOUSE BAND 3 ANION EXCHANGE PROTEIN [M.musculus], expressed sequence A1503023, solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	
1920	24697	NM_017048	u, v, ii	solute carrier family 4 (anion exchanger), member 2, solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	solute carrier family 4 (anion exchanger), member 2, solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	
1969	24859	NM_017206	h, i	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	

TABLE 3

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atty. Ref. 44921-5090-01-WO/2105485
1923	1876	NM_017052	w, x	sorbitol dehydrogenase, sorbitol dehydrogenase 1	ESTs, Highly similar to A54674 L-iditol 2-dehydrogenase [H.sapiens], sorbitol dehydrogenase, sorbitol dehydrogenase 1	
2049	23419	NM_019257	t	splicing factor, arginine/serine-rich 5, splicing factor, arginine/serine-rich 5 (SRp40, HRS)	ESTs, Weakly similar to SFR5 MOUSE SPLICING FACTOR, ARGININE/SERINE-RICH 5 [M.musculus], Mus musculus, clone MGC:36924 IMAGE:4945988, mRNA, complete cds, RIKEN cDNA 1210001E11 gene, RIKEN cDNA 6330415C05 gene, splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor), splicing factor, arginine/serine-rich 4, splicing factor, arginine/serine-rich 5, splicing factor, arginine/serine-rich 5 (SRp40, HRS)	
1948	16681	NM_017136	ii	squalene epoxidase	Homo sapiens cDNA FLJ30795 fis, clone FEBRA2001124, squalene epoxidase	
2294	14542	NM_031596	r	squamous cell carcinoma antigen recognised by T cells, squamous cell carcinoma antigen recognized by T-cells 1		
2294	14543	NM_031596	b, u, v	squamous cell carcinoma antigen recognised by T cells, squamous cell carcinoma antigen recognized by T-cells 1		
865	20924	A1012832	ii, ll	stannin	RIKEN cDNA 2810407J07 gene, stannin	
2491	15707	NM_058208	d	STAT induced STAT inhibitor-2, cytokine inducible SH2-containing protein 2	ESTs, Weakly similar to cytokine inducible SH2-containing protein C1S4 [Mus musculus] [M.musculus], JAK binding protein, RIKEN cDNA 5830401B18 gene, STAT induced STAT inhibitor-4, Socs-5, cytokine inducible SH2-containing protein 2	
1771	21087	NM_012661	cc, dd	steroid sulfatase, steroid sulfatase (microsomal), arylsulfatase C, isozyme S	ESTs, Highly similar to l37186 arylsulfatase D [H.sapiens], ESTs, Weakly similar to STS MOUSE STERYL-SULFATASE PRECURSOR [M.musculus], ESTs, Weakly similar to STS_RAT STERYL-SULFATASE PRECURSOR (STERIOD SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) [R.norvegicus], arylsulfatase E (chondrodysplasia punctata 1), arylsulfatase F, steroid sulfatase, steroid sulfatase (microsomal), arylsulfatase C, isozyme S	
1236	15393	A170663	cc, dd	sterol regulatory element binding transcription factor 2	sterol regulatory element binding factor 1, sterol regulatory element binding factor 2, sterol regulatory element binding transcription factor 2	
1694	17508	L08814	ii	structure specific recognition protein 1	ESTs, Weakly similar to S35637 high mobility group 1 protein homolog - rat (fragment) [R.norvegicus], Mus musculus, clone IMAGE:4948318, mRNA, partial cds, Mus musculus, clone IMAGE:5355658, mRNA, structure specific recognition protein 1	

TABLE 3

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2425	18175	NM_053752	aa, bb	succinate-CoA ligase, GDP-forming, alpha subunit	
2336	4748	NM_031834	s, t, aa, bb	sulfoltransferase family 1A, phenol-preferring, member 1, sulfoltransferase family, cytosolic, 1A, phenol-preferring, member 1	Aryl sulfoltransferase cytosolic, 1A, phenol-preferring, member 3, RIKEN cDNA 1110030E23 gene, sulfoltransferase family 1A, phenol-preferring, member 1, sulfoltransferase family, cytosolic, 1A, phenol-preferring, member 1, sulfoltransferase family, cytosolic, 1A, phenol-preferring, member 2
2336	4749	NM_031834	t, bb	sulfoltransferase family 1A, phenol-preferring, member 1, sulfoltransferase family, cytosolic, 1A, phenol-preferring, member 1	Aryl sulfoltransferase cytosolic, 1A, phenol-preferring, member 3, RIKEN cDNA 1110030E23 gene, sulfoltransferase family 1A, phenol-preferring, member 1, sulfoltransferase family, cytosolic, 1A, phenol-preferring, member 1, sulfoltransferase family, cytosolic, 1A, phenol-preferring, member 2
1922	20875	NM_017050	hh	superoxide dismutase 1, soluble, superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	EST, Weakly similar to SODC MOUSE SUPEROXIDE DISMUTASE [M.musculus], superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
1922	20876	NM_017050	r	superoxide dismutase 1, soluble, superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	EST, Weakly similar to SODC MOUSE SUPEROXIDE DISMUTASE [M.musculus], superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
2164	18098	NM_022947	l	suppressor of K <sup>+</sup> transport defect 3, suppressor of potassium transport defect 3	
2130	4601	NM_022524	l, m	sushi-repeat-containing protein, sushi-repeat-containing protein, X chromosome	ESTs, Weakly similar to down-regulated by v-src gene [Rattus norvegicus] [R.norvegicus], Homo sapiens mRNA; cDNA DKFZp586N2022 (from clone DKFZp586N2022), RIKEN cDNA 1110039C07 gene, RIKEN cDNA 2610001E17 gene, sushi-repeat protein, sushi-repeat-containing protein, sushi-repeat-containing protein, X chromosome
833	15917	A011498	b	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
2027	20440	NM_019166	b, l, m	synaptogyrin 1	ESTs, Moderately similar to SNG1_RAT SYNAPTOGYRIN 1 (P29) [R.norvegicus], synaptogyrin 1, synaptogyrin 3, synaptogyrin 4

TABLE 3					
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
					EST, Weakly similar to JW0105 synaptotagmin 2 alpha protein - mouse [M.musculus], ESTs, Moderately similar to PW0049 synaptotagmin 2 zeta protein - mouse (fragment) [M.musculus], ESTs, Weakly similar to JW0105 synaptotagmin 2 alpha protein - mouse [M.musculus], ESTs, Weakly similar to T42384 inositol-1,4,5-trisphosphate 5-phosphatase [M.musculus], ESTs, Weakly similar to FLJ23105 fis, clone LNG07677, inositol polyphosphate 5-phosphatase, oculocerebrorenal syndrome of Lowe, phosphatidylinositol (4,5) bisphosphate 5-phosphatase homolog; phosphatidylinositol polyphosphate 5-phosphatase type IV, phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A, synaptotagmin 2
2352	1171	NM_032071	y, z	synaptotagmin 2	
2015	20536	NM_019122	b, l, m, u, v	synaptotagmin 3, synaptotagmin III	
1769	9423	NM_012649	j, k, y, z	syndecan 4, syndecan 4 (amphiglycan, ryudocan)	
2250	1265	NM_031124	u, v	syntaxin 3, syntaxin 3A	
2028	7486	NM_019169	n, o	synuclein, alpha, synuclein, alpha (non A4 component of amyloid precursor)	
					ESTs, Weakly similar to S58222 PQ-rich protein [H.sapiens], T-cell death associated gene, pleckstrin homology-like domain, family A, member 1, pleckstrin homology-like domain, family A, member 3, tumor suppressing subtransferable candidate 3, tumor-suppressing subchromosomal transferable fragment 3
1963	19031	NM_017180	p, q	T-cell death associated gene, pleckstrin homology-like domain, family A, member 1	
2620	25593	U26310	gg	tenascin	
					RIKEN cDNA 4833428C18 gene, RIKEN cDNA 4930584N22 gene, hypothetical protein BC007901, testis specific protein kinase 1, testis-specific kinase 1, testis-specific kinase 2
2291	21715	NM_031578	aa	testis specific protein kinase 1, testis-specific kinase 1	
2299	24234	NM_031614	r, y, z, jj, kk	thioredoxin reductase 1	
2299	24235	NM_031614	y, z, kk	thioredoxin reductase 1	
2140	21076	NM_022584	e, w, x	thioredoxin reductase 2	
450	12031	AA893860	y, z	threonyl-tRNA synthetase	
					threonyl-tRNA synthetase
1815	16871	NM_012887	y, ll	thymopoietin	
2077	20816	NM_021261	c	thymosin, beta 10	
					ESTs, Highly similar to THPA_HUMAN THYMOPOIETIN ALPHA [H.sapiens], RIKEN cDNA 5630400D24 gene, thymopoietin
1855	11113	NM_013046	l, k, p, q, u, v, gg	thyrotropin releasing hormone, thyrotropin-releasing hormone	
1855	11114	NM_013046	k, n, o, y, z, kk	thyrotropin releasing hormone, thyrotropin-releasing hormone	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2092	243	NM_021989	h, i, n, o, ll	tissue inhibitor of metalloproteinase 2	Homo sapiens mRNA; cDNA DKFZp761A0617 (from clone DKFZp761A0617), tissue inhibitor of metalloproteinase 2	
229	17236	AA858903	s, t, gg	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	
512	17231	AA924107	ii	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	
697	17232	AA965161	ll	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	
476	23778	AA899854	c	topoisomerase (DNA) II alpha, topoisomerase (DNA) II alpha (170kD)	ESTs, Moderately similar to A40493 DNA topoisomerase [H.sapiens], ESTs, Weakly similar to topoisomerase (DNA) II alpha [Rattus norvegicus] [R.norvegicus], topoisomerase (DNA) II alpha, topoisomerase (DNA) II beta	
2094	23780	NM_022183	jj, kk	topoisomerase (DNA) II alpha, topoisomerase (DNA) II alpha (170kD)	ESTs, Moderately similar to A40493 DNA topoisomerase [H.sapiens], ESTs, Weakly similar to topoisomerase (DNA) II alpha [Rattus norvegicus] [R.norvegicus], topoisomerase (DNA) II alpha, topoisomerase (DNA) II beta	
2378	622	NM_053369	a, j, k	transcription factor 4	EST, Highly similar to TRANSCRIPTION FACTOR 4 [M.musculus], transcription factor 4	
2378	623	NM_053369	r, hh	transcription factor 4	EST, Highly similar to TRANSCRIPTION FACTOR 4 [M.musculus], transcription factor 4	
2079	18729	NM_021578	r	transforming growth factor, beta 1, transforming growth factor, beta 1 (Camurati-Engelmann disease)		
1723	457	M60666	aa	tropomyosin 1 (alpha), tropomyosin 1, alpha	Homo sapiens cDNA FLJ30635 fis, clone CTONG2002520, expressed sequence A1854628, expressed sequence C76867, tropomyosin 4, tuffelin 1	
2018	455	NM_019131	b, u, v	tropomyosin 1 (alpha), tropomyosin 1, alpha	Homo sapiens cDNA FLJ30635 fis, clone CTONG2002520, expressed sequence A1854628, expressed sequence C76867, tropomyosin 4, tuffelin 1	
2018	461	NM_019131	b, l, m	tropomyosin 1 (alpha), tropomyosin 1, alpha	Homo sapiens cDNA FLJ30635 fis, clone CTONG2002520, expressed sequence A1854628, expressed sequence C76867, tropomyosin 4, tuffelin 1	
1773	24854	NM_012676	aa, bb	troponin T2, cardiac	EST, Weakly similar to TRT2 MOUSE TROPONIN T, CARDIAC MUSCLE ISOFORMS [M.musculus], hypothetical protein FLJ10498	



TABLE 3						Atty. Ref. 44921-5090-01-WO/2105485
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1811	24617	NM_012870	ii	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	tumor necrosis factor receptor superfamily, member 11a, tumor necrosis factor receptor superfamily, member 11a, activator of NFKB, tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin), tumor necrosis factor receptor superfamily, member 21, tumor necrosis factor receptor superfamily, member 5, tumor necrosis factor receptor superfamily, member 6b, decoy	
1935	23665	NM_017092	u, v	TYRO3 protein tyrosine kinase, TYRO3 protein tyrosine kinase 3	AXL receptor tyrosine kinase, TYRO3 protein tyrosine kinase, TYRO3 protein tyrosine kinase 3	
2295	19341	NM_031603	h, l	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	ESTs, Highly similar to I38947 14-3-3 protein epsilon isoform [H.sapiens], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	
554	3817	AA926328	p, q	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	ESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX [H.sapiens], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	
1846	25279	NM_013011	p, q	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	ESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX [H.sapiens], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	
1846	3404	NM_013011	p, q	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	ESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX [H.sapiens], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	
					EST, Weakly similar to UCRL_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens], ESTs, Moderately similar to UCRL_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens], RIKEN cDNA 4430402G14 gene, ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	
1712	15049	M24542	aa, bb	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A8	
2477	15125	NM_057105	jj, kk, ll	UDP glycosyltransferase 1 family, polypeptide A6	Mus musculus, Similar to xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I), clone MGC:28643 IMAGE:4224150, mRNA, complete cds, UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1, UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	
133	23828	AA817823	ii	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	
2426	7927	NM_053765	d	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase		

TABLE 3					Human Homologous Sequence Cluster Title	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name		
2023	278	NM_019150	aa, bb	urocortin	urocortin	
2688	19279	Y00350	a, aa, bb, jj, kk	uroporphyrinogen decarboxylase		
1215	6888	A169615	s, t	VAMP (vesicle-associated membrane protein)-associated protein A (33 kDa)	VAMP (vesicle-associated membrane protein)-associated protein A (33kD), vesicle-associated membrane protein, associated protein A (33 kDa)	
1439	16203	A1229196	w, x, cc, dd	vesicle-associated membrane protein 1, vesicle-associated membrane protein 1 (synaptobrevin 1), vesicle-associated membrane protein 2, vesicle-associated membrane protein 2 (synaptobrevin 2)	vesicle-associated membrane protein 1, vesicle-associated membrane protein 2, vesicle-associated membrane protein 4	
1772	16197	NM_012663	j, k	vesicle-associated membrane protein 2, vesicle-associated membrane protein 2 (synaptobrevin 2)		
2472	23250	NM_057097	f, g	vesicle-associated membrane protein 3, vesicle-associated membrane protein 3 (cellubrevin)	ESTs, Weakly similar to vesicle-associated membrane protein 3 [Rattus norvegicus] [R.norvegicus], vesicle-associated membrane protein 3, vesicle-associated membrane protein 3 (cellubrevin), vesicle-associated membrane protein 4	
2026	24362	NM_019156	jj, kk	vitronectin, vitronectin (serum spreading factor, somatomedin B, complement S-protein)		
1956	21975	NM_017154	d, e, j, k, n, o, y, z, kk	xanthine dehydrogenase, xanthine dehydrogenase		
1960	20919	NM_017172	a	zinc finger protein 36, C3H type-like 1	ESTs, Weakly similar to S10471 cMG1 protein - rat [R.norvegicus], zinc finger protein 36, C3H type-like 1, zinc finger protein 36, C3H type-like 2	
2511	25730	NM_133290	j, k, p, q	zinc finger protein 36, zinc finger protein 36, C3H type, homolog (mouse)	zinc finger protein 36, zinc finger protein 36, C3H type, homolog (mouse)	
2541	8692	NM_134387	hh		2,4-dienoyl CoA reductase 1, mitochondrial, 2,4-dienoyl CoA reductase 2, peroxisomal, 2,4-dienoyl-Coenzyme A reductase 2, peroxisomal, RIKEN cDNA 1810027P18 gene, putative peroxisomal 2,4-dienoyl-CoA reductase	
177	19451	AA819788	c		28kD interferon responsive protein, RIKEN cDNA 5830458K16 gene	
1646	23219	AJ000347	n, o		3'(2), 5'-bisphosphate nucleotidase 1, ESTs, Moderately similar to INPP MOUSE INOSITOL POLYPHOSPHATE 1-PHOSPHATASE [M.musculus], bisphosphate 3'-nucleotidase 1, hypothetical protein FLJ20421, inositol polyphosphate-1-phosphatase	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID No.	GenBank Acc.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1715	15580	M33648	y, z		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2, 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	
2465	17739	NM_053995	g		3-hydroxybutyrate dehydrogenase (heart, mitochondrial), ESTs, Weakly similar to BDH_RAT D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor (BDH) (3-hydroxybutyrate dehydrogenase) [R.norvegicus], RIKEN cDNA 0610039E24 gene, RIKEN cDNA 2310032J20 gene, retinol dehydrogenase 7, retinol dehydrogenase type 5	
889	21950	A1013861	a, h, l		3-hydroxyisobutyrate dehydrogenase, ESTs, Highly similar to D3H1_HUMAN 3-HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (HIBADH) [H.sapiens], RIKEN cDNA 3930401K13 gene	
2060	1238	NM_019333	gg		6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1, 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4, ESTs, Moderately similar to F26L MOUSE 6PF-2-KFRU-2,6-PZASE LIVER ISOZYME [M.musculus]	
2076	13486	NM_020306	aa, bb		a disintegrin and metalloproteinase domain 17, a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	
2323	20724	NM_031753	d		activated leucocyte cell adhesion molecule, activated leukocyte cell adhesion molecule	
2198	938	NM_024486	u, v		activin A receptor, type 1, activin A receptor, type I	
2083	19661	NM_021686	n		activin receptor interacting protein 1, connector enhancer of KSR2, expressed sequence AA407180, phosphoinositide-binding protein PIP3-E	
472	4636	AA899491	e		adaptor-related protein complex 1, mu 1 subunit	
2532	1271	NM_133593	kk	a, ee, ff, jj,	adaptor-related protein complex 3, mu 1 subunit, adaptor-related protein complex AP-3, mu 1 subunit	
2317	24081	NM_031708	e		adhesion regulating molecule 1	
1445	15212	A1229753	p, q, t, y, z, ee, ff		ADP-ribosylation factor 1, ADP-ribosylation factor 2, ARF protein	
2178	1742	NM_024150	p, q, y, ee, ff		ADP-ribosylation factor 1, ADP-ribosylation factor 2, ARF protein	
2127	4145	NM_022518	jj, kk		ADP-ribosylation factor 1, ADP-ribosylation-like 6, ESTs, Weakly similar to ADP-RIBOSYLATION FACTOR 1 [M.musculus], expressed sequence T25534	
2127	4151	NM_022518	b, l, m		ADP-ribosylation factor 1, ADP-ribosylation-like 6, ESTs, Weakly similar to ADP-RIBOSYLATION FACTOR 1 [M.musculus], expressed sequence T25534	
2179	17517	NM_024151	f		ADP-ribosylation factor 4	

TABLE 3

SEQ ID		GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Atty. Ref. 44921-5090-01-WO/2105485
2180		21696NM_024152	y, z		ADP-ribosylation factor 6, ESTs, Weakly similar to ARF6_HUMAN ADP-RIBOSYLATION FACTOR 6 [M.musculus], ESTs, Weakly similar to ARF6_HUMAN ADP-ribosylation factor 6 [R.norvegicus], RIKEN cDNA 1110033P22 gene, RIKEN cDNA 2310075M17 gene, RIKEN cDNA 9130014L17 gene, SAR1 protein, SAR1a gene homolog (S. cerevisiae), hypothetical protein FLJ22595	
552		20327AA926265	cc, dd		ADP-ribosylation factor-like 5, ADP-ribosylation-like 6, expressed sequence T25534, hypothetical protein DKFZp434L1123 similar to mouse Arf6	
2480		727NM_057123	s, t		AFG3 ATPase family gene 3-like 1 (yeast), BCS1-like (yeast), EST, Weakly similar to PRS4_HUMAN 26S protease regulatory subunit 4 (P26S4) [M.musculus], ESTs, Highly similar to PRS4_HUMAN 26S protease regulatory subunit 4 (P26S4) [H.sapiens], Homo sapiens cDNA FLJ31926 fis, clone NT2RP7005502, moderately similar to Homo sapiens mRNA for paraplegin-like protein, protease (prosome, macropain) 26S subunit, ATPase 1, proteasome (prosome, macropain) 26S subunit, ATPase, 1	
2418		2063NM_053682	e		AFG3 ATPase family gene 3-like 2 (yeast), AFG3(ATPase family gene 3)-like 1 (yeast), Mus musculus, clone IMAGE:5040761, mRNA, partial cds, YME1-like 1 (S. cerevisiae), spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)	
1403		3094AI179700	b, l, m		Agrin, ESTs, Weakly similar to A38096 perlecan precursor [H.sapiens], ESTs, Weakly similar to BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR [M.musculus], ESTs, Weakly similar to PGBM_HUMAN BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR [H.sapiens], Mus musculus, clone IMAGE:3494258, mRNA, partial cds, heparan sulfate proteoglycan 2 (perlecan), perlecan (heparan sulfate proteoglycan 2), serine protease inhibitor, Kazal type, 5, sialoadhesin, transmembrane protein with EGF-like and two follistatin-like domains 1	
280		16074AA874874	p, q		alcohol dehydrogenase 5, alcohol dehydrogenase 5 (class II), chi polypeptide	
2343		24644NM_031972	cc, dd		aldehyde dehydrogenase 3 family, member B1, aldehyde dehydrogenase 3 family, member B2, aldehyde dehydrogenase 3 family, member A1, aldehyde dehydrogenase family 3, subfamily A1	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
485	4725	AA900290	t, y, z, ee, ff		Alpha-2-macroglobulin, CCR4 carbon catabolite repression 4-like (S. cerevisiae), ESTs, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], Homo sapiens, clone MGC:1119 IMAGE:2959975, mRNA, complete cds, Mus musculus, clone MGC:29037 IMAGE:3598248, mRNA, complete cds, Mus musculus, clone MGC:29167 IMAGE:5052974, mRNA, complete cds, alpha-2-macroglobulin, carbon catabolite repression 4 homolog (S. cerevisiae), pregnancy-zone protein	
2171	8269	NM_023103	b, l, m		alpha-2-macroglobulin, murinoglobulin 1, murinoglobulin 2, murinoglobulin, pseudogene 1	
1876	16649	NM_013132	c, gg		annexin A5	
222	15260	AA858518	f, g		APC11 anaphase promoting complex subunit 11 homolog (yeast), ESTs, Highly similar to T51146 ring-box protein 1 [H.sapiens], ESTs, Weakly similar to T51146 ring-box protein 1 [H.sapiens], ring finger protein 7, ring-box 1	
687	18830	AA964496	a, z		ARF2 actin-related protein 2 homolog (Yeast), ARF3 actin-related protein 3 homolog (Yeast), EST, Weakly similar to ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin) [R.norvegicus], ESTs, Highly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1 [M.musculus], ESTs, Weakly similar to A29861 actin gamma [H.sapiens], ESTs, Weakly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1 [M.musculus], Homo sapiens cDNA FLJ31247 fis, clone KIDNE2005296, weakly similar to ACTIN, CYTOPLASMIC 1, Homo sapiens cDNA FLJ32120 fis, clone PEBLM1000068, highly similar to ACTIN, CYTOPLASMIC TYPE 5, Homo sapiens mRNA; cDNA DKFZp434B2115 (from clone DKFZp434B2115), RIKEN cDNA 1700052K15 gene, actin, beta, actin, beta, cytoplasmic, calcitonin gene-related peptide-receptor component protein, expressed sequence AV259599	

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
					Human Homologous Sequence Cluster Title	
					Human Homologous Sequence Cluster Title	
1137	18831	A1104357	bb		Human Homologous Sequence Cluster Title	
230	5867	AA858953	kk		Human Homologous Sequence Cluster Title	
1383	15091	A1178740	cc, dd		Human Homologous Sequence Cluster Title	
2559	7395	NM_138883	r		Human Homologous Sequence Cluster Title	
2509	20738	NM_131907	c		Human Homologous Sequence Cluster Title	
2448	20939	NM_053884	gg		Human Homologous Sequence Cluster Title	

TABLE 3

SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
1209	22661	AI169265	gg		ATPase, H <sup>+</sup> transporting, lysosomal interacting protein 1, EST, Weakly similar to I54197 hypothetical protein [H.sapiens], ESTs, Weakly similar to VAS1_RAT Vacuolar ATP synthase subunit S1 precursor (V-ATPase S1 subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45 subunit) (C7-1 protein) [R.norvegicus], Homo sapiens cDNA FLJ12563 fis, clone NT2RM400820, weakly similar to VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34), expressed sequence AW108110
2327	16178	NM_031785	f		ATPase, H <sup>+</sup> transporting, lysosomal interacting protein 1, EST, Weakly similar to I54197 hypothetical protein [H.sapiens], ESTs, Weakly similar to VAS1_RAT Vacuolar ATP synthase subunit S1 precursor (V-ATPase S1 subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45 subunit) (C7-1 protein) [R.norvegicus], Homo sapiens cDNA FLJ12563 fis, clone NT2RM400820, weakly similar to VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34), expressed sequence AW108110
2296	20840	NM_031604	cc, dd		ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit A isoform 4, ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a isoform 1, ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a isoform 2, ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a isoform 4, EST, Weakly similar to B38656 vacuolar proton pump 116K chain - rat [R.norvegicus], ESTs, Moderately similar to B38656 vacuolar proton pump 116K chain - rat [R.norvegicus]
1871	23709	NM_013113	f, g		ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1 polypeptide
1871	23710	NM_013113	hh		ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1 polypeptide
1560	3650	AI235738	r		ATP-binding cassette, sub-family C (CFTRMRP), member 4, ATP-binding cassette, sub-family C (CFTRMRP), member 9, ESTs, Weakly similar to ATP-binding cassette, sub-family C, member 9, isoform c; sulfonylurea-binding protein 2; sulfonylurea receptor 2 [Mus musculus] [M.musculus], Homo sapiens cDNA FLJ31957 fis, clone NT2RPP7007381, highly similar to Sulfonylurea receptor 2A, Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330439B14:ATP-binding cassette, sub-family C (CFTRMRP), member 9, full insert sequence
1217	24146	AI169668	ii		ATP-binding cassette, sub-family F (GCN20), member 2

TABLE 3					Atty. Ref. 44921-5090-01-WO/2105485	
SEQ ID	GLGC ID	GenBank Acc. No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
248	20582	AA859688	w, hh		AU RNA binding protein/enoyl-Coenzyme A hydratase, AU RNA binding protein/enoyl-coenzyme A hydratase, ESTs, Weakly similar to I37195 AU-specific RNA-binding protein / enoyl-CoA hydratase homolog [H.sapiens], Mus musculus, Similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase, clone MGC:31364 IMAGE:4238881, mRNA, complete cds, RIKEN cDNA 1300017C12 gene, uncharacterized hypothalamus protein HCDASE	
798	22545	A1009747	a		B-cell translocation gene 1, anti-proliferative, ESTs, Highly similar to TOB1_HUMAN TOB1 PROTEIN [H.sapiens], transducer of ERBB2, 1, transducer of ERBB2, 2, transducer of ErbB-2.1	
2055	23679	NM_019290	p, q		B-cell translocation gene 3, BTG family, member 3	
2500	23033	NM_080888	r		BCL2/adenovirus E1B 19 kDa-interacting protein 3-like, BCL2/adenovirus E1B 19kD interacting protein 3-like	
2153	17757	NM_022698	cc, dd		BCL2-antagonist of cell death, Bcl-associated death promoter	
781	21632	A1009167	a, y, z, ee, ff		BCL2-associated athanogene 2	
1493	15171	A1231792	ee, ff		BCL2-associated athanogene 3, BCL2-associated athanogene 5, Bcl2-associated athanogene 3, RIKEN cDNA 1700081D05 gene	
558	22677	AA942718	s, t, kk		BCL2-related ovarian killer, Bcl2-like	
660	23957	AA957123	c		brain expressed, X-linked 1, hypothetical protein FLJ10097	
1466	22387	A1230753	f, g		brain protein i3	
412	11997	AA892828	f, h, l		branched chain ketoacid dehydrogenase E1, beta polypeptide, pyruvate dehydrogenase (lipoamide) beta	
1313	5876	A1176117	hh		branched chain ketoacid dehydrogenase E1, beta polypeptide, pyruvate dehydrogenase (lipoamide) beta	
2209	21801	NM_030987	cc, dd, ii		BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast), ESTs, Weakly similar to guanine nucleotide-binding protein, beta-1# subunit [Rattus norvegicus] [R.norvegicus], Mus musculus, clone MGC:7934 IMAGE:3583848, mRNA, complete cds, budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae), guanine nucleotide binding protein, beta 1, neural precursor cell expressed, developmentally down-regulated gene 1	